

STIC-Biotech/ChemLib

129094

From: Slobodyansky, Elizabeth
Sent: Wednesday, August 04, 2004 5:04 PM
To: STIC-Biotech/ChemLib
Subject: 09/430,029

Please search for case 09/430,029:

removed EG

SEQ ID NO: 8 against commercial ~~and interference~~ databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652
REM 3A65
571-272-0941
MAILBOX 3C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: *8/5/04*
Date Completed: *8/5/04*
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: *DS*
WWW/Internet: _____
Other(Specify): _____

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 5, 2004, 13:09:29 ; Search time 54 Seconds
(without alignments)
617.419 Million cell updates/sec

Title: US-09-430-029-8

Perfect score: 619

Sequence: 1 MDAGRVCVTIAQTDERYA.....RLRKPFCGACAGTAANK 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	619	100.0	118	3	AAY84822 Amino aci
2	418.5	67.6	111	3	AAY96262 R. eutrop
3	322	52.0	119	7	AAO23395 Pseudomon
4	259.5	41.9	112	4	AAG64662 Hydroxyin
5	228.5	36.9	101	2	Aaw98976 Alcaligen
6	144.5	23.3	342	2	AAR66216 Nocardia
7	144.5	23.3	342	2	AAR81472 Nocardia
8	130.5	21.1	343	6	ABU22750 Protein e
9	129.5	20.9	329	2	AAM80338 Oxidase a
10	126.5	20.4	343	6	ABU21309 Protein e
11	124.5	20.1	343	6	ABU19841 Protein e
12	123	19.9	346	6	ABP97021 Sphingomo
13	123	19.9	346	6	ABP97025 Sphingomo
14	120	19.4	366	6	ABU41589 Protein e
15	117	18.9	368	6	ABU40068 Protein e
16	113	18.3	366	6	ABU38911 Protein e
17	111	17.9	405	6	ABP79217 N. gonorr
18	110	17.8	92	2	AAM14449 CarB gene
19	109.5	17.7	336	6	ABP78930 Protein e
20	109.5	17.7	336	6	ABU37353 Protein e
21	109	17.6	348	6	ABU22973 Protein e
22	105	17.0	350	2	AAR05385 Xylene ox
23	105	17.0	350	6	ABP97023 Pseudomon
24	104.5	16.9	326	4	AAB60228 C Glutami
25	103.5	16.7	512	4	AAG92388

ALIGNMENTS

RESULT 1
AAY84822

ID AAY84822 standard; protein; 118 AA.

AC AAY84822;

DT 08-AUG-2000 (first entry)

DE Amino acid sequence of toluene monooxygenase TomQ.

KM Toluene monooxygenase; TomK; TomL; TomM; TomO; TomP; TomQ; toluene;
KW ortho-cresol; 3-methylcatechol; chlorinated compound;
KW aliphatic hydrocarbon; trichloroethylene; dichloroethylene; phenol;
KW aromatic compound; benzene; cresol; environmental remediation.

OS Burkholderia cepacia.

FN EP999274-A2.

PD 10-MAY-2000.

PF 02-NOV-1999; 99EP-00121681.

PR 30-OCT-1998; 98JP-00310801.

PA (CANO) CANON KK.

PI Yano T, Nomoto T, Imamura T;

DR WPI; 2000-306010/27.

DR N-PSDB; AAA14845.

PT Novel DNA fragment encoding a toluene monooxygenase, useful for degrading
a chlorinated aliphatic hydrocarbon compound, or an aromatic compound,
e.g. in environmental remediation.

PS Claim 46; Page 45; 52pp; English.

CC AAY84816-22 represent toluene monooxygenase enzymes TomK, TomL, TomM,
TomN, TomO, TomP, and TomQ, respectively. The enzymes oxidise toluene to
ortho-cresol and 3-methylcatechol. The toluene monooxygenase has a high
efficiency in degrading aromatic and volatile organic chlorinated
compounds. The nucleic acids are useful for the recombinant production of
toluene monooxygenase. Toluene monooxygenase is useful for degrading a
chlorinated aliphatic hydrocarbon compound (e.g. trichloroethylene (TCE)
or dichloroethylene (DCE)), or an aromatic compound (e.g. toluene,
benzene, phenol, and cresol), e.g. in environmental remediation. It is
especially useful for purifying air polluted with chlorinated aliphatic

ABU40855 Protein e
ABU29472 Burkholde
ABU21907 Protein e
ABU38023 Protein e
ABU25632 Protein e
ABU61631 Protein e
ABU20107 Protein e
ABU78834 N. gonorr
ABU50056 Protein e
ADA35088 Acinetoba
ABU31645 Protein e
ABU21203 Protein e
ABU48037 Protein e
AAY35534 Chlamydia
ABU27042 Protein e
ABU2741 Protein e
ABU15018 Protein e
AAU23193 Novel hum
AAY96261 R. eutrop
AAW98975 Alcaligen

CC hydrocarbon compounds

XX Sequence 118 AA;

Query Match 100.0%; Score 619; DB 3; Length 118;

Best Local Similarity 100.0%; Pred. No. 1.5e-63;

Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAGRVCGTIVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAV 60

DB 1 MDAGRVCGTIVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAV 60

QY 61 RKLGPISRAHVSABEENDGYALACRVVDPDGVLEVAGRLRKPFPCGACAGTAAINK 118

DB 61 RKLGPISRAHVSABEENDGYALACRVVDPDGVLEVAGRLRKPFPCGACAGTAAINK 118

RESULT 2

AAAY96262

ID AAY96262 standard; protein; 111 AA.

XX AC AAY96262;

DT 12-SEP-2003 (revised)

DT 11-SEP-2000 (first entry)

XX R. eutropha toluene monooxygenase TomQ polypeptide.

XX Toluene monooxygenase; carcinogen; halogenated aliphatic hydrocarbon;

KW halogenated aromatic hydrocarbon; environmental pollution; TomQ;

KW environmental remediation; enzyme.

XX Ralstonia eutropha; strain TB64.

OS EP1006191-A2.

PN 07-JUN-2000.

XX 03-DEC-1999; 99EP-00124209.

XX 03-DEC-1998; 98JP-00344506.

XX (CANO) CANON KK.

XX Yano T, Nomoto T, Imamura T;

XX WPI: 2000-378265/33.

DR N-PSDB; AAA30292.

XX New polynucleotide encoding toluene monooxygenase for generating

PT transformants useful for decontaminating environments polluted with e.g.

PT aromatic hydrocarbons.

XX Claim 38; Page 48; 54pp; English.

XX The present sequence is the Ralstonia eutropha toluene monooxygenase TomQ

CC polypeptide. This peptide is encoded by a DNA fragment of about 5.3 Kb

CC which also contains six other coding sequences encoding other toluene

CC monooxygenase polypeptides (AAA30292). The DNA fragment is useful for

CC transforming microbial cells to confer them with toluene monooxygenase

CC activity. These cells are in turn useful for decontaminating environments

CC polluted with halogenated aliphatic compounds e.g. tetrachloroethylene

CC (PCE), trichloroethylene (TCE) and dichloroethylene (DCE) and/or aromatic

CC hydrocarbons e.g. toluene, benzene, phenol, cresol. These pollutants are

CC considered to be potential carcinogens. The present sequence is not

CC essential for toluene monooxygenase activity. (Updated on 12-SEP-2003 to

CC standardise OS field)

XX Sequence 111 AA;

QY Query Match 67.6%; Score 418.5; DB 3; Length 111;

Best Local Similarity 76.7%; Pred. No. 2.3e-40;

Matches 79; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY

DB

QY

DB

RESULT 3

AAO23395

ID AAO23395 standard; protein; 119 AA.

XX AC AAO23395;

XX 06-NOV-2003 (first entry)

XX Pseudomonas plasmid CT14 ORF1 bacterial ferredoxin protein.

XX Bacterial plasmid; CT14; aromatic degradation; heavy metal resistance;

KW catechol; toluene degradative pathway; mercury; ferredoxin; ORF1.

XX Pseudomonas sp.

XX US6548292-B1.

XX 15-APR-2003.

XX 20-NOV-2000; 2000US-00716865.

XX 23-NOV-1999; 99US-0167062P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Bramucci MG, Chen MW, Nagarajan V;

XX WPI: 2003-566606/53.

XX N-PSDB; AAL56814.

XX New bacterial plasmid isolated from Pseudomonas CT14, designated as

PT pCT14, useful for degrading aromatic compounds, and in plasmid

PT replication, or partitioning of replicated plasmids to daughter cells

PT during cell division.

XX Example 4; Col 31-34; 60pp; English.

XX This invention relates to a novel isolated bacterial plasmid designated

CC CT14, isolated from a wastewater bacterial Pseudomonas strain.

CC Specifically, the plasmid pCT14 carries the genes necessary for

CC replication and stability in a host, as well as genes encoding enzymes

CC for the degradation of various aromatic substrates including catechols

CC and other intermediates in the toluene degradative pathway. Furthermore,

CC pCT14 carries heavy metal resistance genes and is useful for reducing the

CC level of mercury in a contaminated environment. As for other bacterial

CC plasmids, pCT14 also carries genes that are used for plasmid replication,

CC partitioning of replicated plasmids to daughter cells during cell

CC division and transposition of insertion sequences or transposons. This

CC polypeptide sequence is the Pseudomonas pCT14 ORF1 ferredoxin protein,

CC which reactivates the catechol dioxygenase enzyme encoded by ORF2 of the

XX invention

XX Sequence 119 AA;

QY Query Match 52.0%; Score 322; DB 7; Length 119;

Best Local Similarity 56.4%; Pred. No. 3.6e-29;

Matches 62; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISR 68

8 TVRVAQTGESFSCTAGESLLAGMAKLGRRGIPVGCINGCGVCKVRVLSGDVRKLGPVSR 67

69 AHVSABEENDGYALACRVVDPDGVLEVAGRLRKPFPCGMACA 111

68 AHVSABEELGYTLACRVAPQGDVLEVAGMKQKPLC---CA 107

9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISR 68

10 SVHVMQTGETFPFCATDESLLQGLRGRGIPVGCINGCGVCKVRVIEGQCRLGPVSR 69

69 AHVSABEENDGYALACRVVDPDGVLEVAGRLRKPFPCGMACAGTAAINK 118

Thu Aug 5 15:10:14 2004

us-09-430-029-8.rag

XX PS Claim 2; Page 4-5; 30pp; Japanese.

XX CC E.coli transformed with the DNA sequence AAQ79569 are able to catalyze

XX CC the epoxidation of alkenes. The DNA is derived from Nocordia corallina

XX CC and comprises 4 open reading frames. ORFs amoA and amoC encode subunits 1

XX CC and 2 of the alkene monooxygenase enzyme and ORF amoD encodes a reductase

XX CC capable of transferring electrons from NADH coenzyme to a monooxygenase.

XX CC (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 342 AA;

Query Match 23.3%; Score 144.5; DB 2; Length 342;

Best Local Similarity 38.6%; Pred. No. 4.6e-08;

Matches 39; Conservative 13; Mismatches 44; Indels 5; Gaps 4;

QY 9 TTTTAQTDERVACVSGESLLAGMAKLGRRGIPVGLNGGCGVKRVLRGAVRKLGPISR 68

Db 3 TINQPSHESYSCDEGESLLDG-ALRNSLLKYGCKHGCGTCKVRLDGDVEEPGS-SF 60

QY 69 AHVSAEENDGYALACRVVP--DGDVELEVAGRLRKPPFCG 107

Db 61 ALTPEDREND-VILACASVPLEPCTIDVEPSGLTEEEFFSG 100

RESULT 7

AA81472

ID AAR81472 standard; protein; 342 AA.

AC AAR81472;

XX 16-OCT-2003 (revised)

DT 07-AUG-1996 (first entry)

XX Nocordia corallina alkene mono-oxygenase gene product, amoD.

XX Alkene mono-oxygenase; indole; indigo production; biosynthesis;

KW microbial oxidation; dye.

OS Gordonia rubripertinctus; B-276.

XX JP08023988-A.

XX 30-JAN-1996.

XX 08-JUL-1994; 94JP-00179688.

XX 08-JUL-1994; 94JP-00179688.

XX (NIHA) JAPAN ENERGY CORP.

XX WPI; 1996-133426/14.

XX N-PSDB; AAT17418.

XX Prepn. of indigo by a microbiological method - by culturing a microbe

XX PT having alkene monooxygenase activity to oxidise indole to indigo.

XX Claim 5; Page 8-9; 11pp; Japanese.

XX AAR81469-R81472 are protein products of the Nocordia corallina strain B-

XX 276 alkene mono-oxygenase gene. The gene encodes 4 protein products amoA,

XX amoB, amoC and amoD derived from the 3 different reading frames of the

XX operon. The gene is useful for the production of indigo via oxidation of

XX indole. Nocordia corallina can be cultured in a medium contg. indole and

XX will readily oxidise the indole yielding indigo into the culture medium.

XX E. coli may also be transformed with the alkene mono-oxygenase gene and

XX used as above to efficiently produce indigo by microbial oxidation.

XX (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 342 AA;

Query Match 23.3%; Score 144.5; DB 2; Length 342;

Best Local Similarity 38.6%; Pred. No. 4.6e-08;

Matches 39; Conservative 13; Mismatches 44; Indels 5; Gaps 4;

QY 9 TTTTAQTDERVACVSGESLLAGMAKLGRRGIPVGLNGGCGVKRVLRGAVRKLGPISR 68

Db 3 TINQPSHESYSCDEGESLLDG-ALRNSLLKYGCKHGCGTCKVRLDGDVEEPGS-SF 60

QY 69 AHVSAEENDGYALACRVVP--DGDVELEVAGRLRKPPFCG 107

Db 61 ALTPEDREND-VILACASVPLEPCTIDVEPSGLTEEEFFSG 100

RESULT 8

ABU22750

ID ABU22750 standard; protein; 343 AA.

AC ABU22750;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #8277.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Burkholderia mallei.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA26620.

XX New antisense nucleic acids, useful for identifying proteins or screening

XX for homologous nucleic acids required for cellular proliferation to

XX isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 50674; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

XX the 6213 antisense sequences given in the specification where expression

XX of the nucleic acid inhibits proliferation of a cell. Also included are:

XX (1) a vector comprising a promoter operably linked to the nucleic acid

XX encoding a polypeptide whose expression is inhibited by the antisense

XX nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX polypeptide or its fragment whose expression is inhibited by the

XX antisense nucleic acid; (4) an antibody capable of specifically binding

XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX proliferation or the activity of a gene in an operon required for

XX proliferation; (7) identifying a compound that influences the activity of

XX the gene product or that has an activity against a biological pathway

XX required for proliferation, or that inhibits cellular proliferation; (8)

XX identifying a gene required for cellular proliferation or the biological

XX pathway in which a proliferation-required gene or its gene product lies

XX on a gene on which the test compound that inhibits proliferation of an

XX organism acts; (9) manufacturing an antibiotic; (10) profiling a

XX compound's activity; (11) a culture comprising strains in which the gene

XX product is overexpressed or underexpressed; (12) determining the extent

XX to which each of the strains is present in a culture or collection of

XX strains; or (13) identifying the target of a compound that inhibits the

XX proliferation of an organism. The antisense nucleic acids are useful for

Matches 39; Conservative 13; Mismatches 44; Indels 5; Gaps 4;

QY 9 TTTTAQTDERVACVSGESLLAGMAKLGRRGIPVGLNGGCGVKRVLRGAVRKLGPISR 68

Db 3 TINQPSHESYSCDEGESLLDG-ALRNSLLKYGCKHGCGTCKVRLDGDVEEPGS-SF 60

QY 69 AHVSAEENDGYALACRVVP--DGDVELEVAGRLRKPPFCG 107

Db 61 ALTPEDREND-VILACASVPLEPCTIDVEPSGLTEEEFFSG 100

RESULT 8

ABU22750

ID ABU22750 standard; protein; 343 AA.

AC ABU22750;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #8277.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Burkholderia mallei.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA26620.

XX New antisense nucleic acids, useful for identifying proteins or screening

XX for homologous nucleic acids required for cellular proliferation to

XX isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 50674; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

XX the 6213 antisense sequences given in the specification where expression

XX of the nucleic acid inhibits proliferation of a cell. Also included are:

XX (1) a vector comprising a promoter operably linked to the nucleic acid

XX encoding a polypeptide whose expression is inhibited by the antisense

XX nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX polypeptide or its fragment whose expression is inhibited by the

XX antisense nucleic acid; (4) an antibody capable of specifically binding

XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX proliferation or the activity of a gene in an operon required for

XX proliferation; (7) identifying a compound that influences the activity of

XX the gene product or that has an activity against a biological pathway

XX required for proliferation, or that inhibits cellular proliferation; (8)

XX identifying a gene required for cellular proliferation or the biological

XX pathway in which a proliferation-required gene or its gene product lies

XX on a gene on which the test compound that inhibits proliferation of an

XX organism acts; (9) manufacturing an antibiotic; (10) profiling a

XX compound's activity; (11) a culture comprising strains in which the gene

XX product is overexpressed or underexpressed; (12) determining the extent

XX to which each of the strains is present in a culture or collection of

XX strains; or (13) identifying the target of a compound that inhibits the

XX proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 343 AA;

Query Match 21.1%; Score 130.5; DB 6; Length 343;
 Best Local Similarity 33.7%; Pred. No. 1.9e-06;
 Matches 31; Conservative 19; Mismatches 37; Indels 5; Gaps 3;
 QY 10 VTIAQTERVACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISRA 69
 DB 5 VTLKSGRQFOVEADETVLAALRQNVH-LPYCKNGAGSGCKGTIVQGQPEQ-GPHSAS 62
 QY 70 HVSAEEENDGYALACRVVDPGDVEL---EVAG 98
 DB 63 ALSNDERTRGLALCCSKPSDLEVDVRETAG 94

RESULT 9
 AAW80338
 ID AAW80338 standard; protein; 329 AA.
 XX
 AC AAW80338;

DT 12-JAN-1999 (first entry)

XX Oxidase amino acid protein.

XX Oxidase; dioxin removal.

XX Pseudomonas sp.

XX JP10257895-A.

XX 29-SEP-1998.

XX 18-MAR-1997; 97JP-00084401.

XX 18-MAR-1997; 97JP-00084401.

XX (ASAH) ASAH KASEI KOGYO KK.

XX WPI; 1998-575906/49.

XX N-PSDB; AAV68080.

XX Oxidase gene derived from a microbe for removal of dioxin - converts
 PT hetero:poly:cyclic aromatic hydrocarbon to a benzoic acid homolog.

XX Example 2; Page 12-13; 15pp; Japanese.

XX The present sequence represents an oxidase which is derived from a
 CC microbe and converts a heteropolycyclic aromatic hydrocarbon to a benzoic
 CC acid homologue. The oxidase is used in a method for the removal of dioxin
 CC in which dibenzo-p-dioxin is converted to a diphenyl ether triol

XX Sequence 329 AA;

Query Match 20.9%; Score 129.5; DB 2; Length 329;
 Best Local Similarity 39.0%; Pred. No. 2.4e-06;
 Matches 30; Conservative 11; Mismatches 35; Indels 1; Gaps 1;

QY 21 CVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISRAHVSAEENDGY 80

DB 14 CGSGKSLVSAALNG-IGFPYECASGGCGVCKFELLEGNNVQSMWPDAPGLSSRDREKGNR 72

QY 81 ALACRVVDPGDVELEVA 97

DB 73 HLACQCVALSRLRIKVA 89
 RESULT 10
 ABU21309
 ID ABU21309 standard; protein; 343 AA.
 XX
 AC ABU21309;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #6836.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Burkholderia fungorum.
 XX
 FN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-USO09107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wali D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA25179.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 49233; 1766pp; English.
 CC
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained


```
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 69513; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 366 AA;
XX
XX Query Match 19.4%; Score 120; DB 6; Length 366;
XX Best Local Similarity 37.2%; Pred. No. 3.4e-05;
XX Matches 32; Conservative 9; Mismatches 41; Indels 4; Gaps 2;
XX
XX QY 10 VTIAQDERYACVSGESLLAGMAKLGRRGIPVGLNGGCGVKVRVLRGAVRKLGPISRA 69
XX Db 284 VFETDTGKSIKRVAPGETVHAAAKVGLM-IPKACGMGICGTCVKWKLGSVEVM--EHNG 339
XX
XX QY 70 HVSAAEENDGYALACRVVDPGDVELE 95
XX Db 340 GITDEDVARGYILSCCSVPKGDVRIE 365
XX
XX RESULT 15
XX ID ABU40068
XX XX ABU40068 standard; protein; 368 AA.
XX AC ABU40068;
XX XX
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #25595.
XX XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Pseudomonas putida.
XX PN WO200277183-A2.
XX XX
XX PD 03-OCT-2002.
XX XX
XX PF 21-MAR-2002; 2002WO-US009107.
XX XX
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX
```

```
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
(ELIT-) ELITRA PHARM INC.
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
WPT; 2003-029926/02.
N-ESDB; ACA43938.
New antisense nucleic acids, useful for identifying proteins or screening
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
Claim 25; SEQ ID NO 67992; 1766pp; English.
The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a gene that influences the activity of
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than S. aureus, S. typhimurium,
K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 368 AA;
Query Match 18.9%; Score 117; DB 6; Length 368;
Best Local Similarity 40.3%; Pred. No. 7.6e-05;
Matches 29; Conservative 10; Mismatches 29; Indels 4; Gaps 2;
QY 24 GESLLAGMAKLGRRGIPVGLNGGCGVKVRVLRGAVRKLGPISRAHVSAAEENDGYALA 83
Db 300 GETVHAAAKVGLM-IPKACGMGICGTCVKVLGGVEVM---EHNGGITEDEAEGYILS 355
QY 84 CRVVPDGDVELE 95
Db 356 CCSVPKGDVRIID 367
Search completed: August 5, 2004, 13:15:40
Job time : 57 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 5, 2004, 13:04:13 ; Search time 18 Seconds
(without alignments)
338.437 Million cell updates/sec

Title: US-09-430-029-8
Perfect score: 619
Sequence: 1 MDAGRVCIVTIAQTDERYA.....RLRKPFPCGACAGTAANK 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	418.5	67.6	111	4	US-09-453-956-8
2	322	52.0	119	4	US-09-716-865-2
3	144.5	23.3	342	1	US-08-499-215-5
4	113	18.3	391	4	US-09-252-991A-17118
5	111	17.9	387	4	US-09-489-039A-14027
6	110	17.8	92	2	US-08-737-825-7
7	104.5	16.9	326	6	5171684-7
8	103	16.6	353	4	US-09-543-681A-7190
9	96	15.5	358	4	US-09-328-352-6375
10	94.5	15.3	411	4	US-09-543-681A-5480
11	92.5	14.9	339	4	US-09-489-039A-12074
12	91	14.7	377	4	US-09-489-039A-9429
13	90.5	14.6	431	4	US-09-198-452A-952
14	88	14.2	352	4	US-09-453-956-7
15	88	14.2	381	4	US-09-489-039A-12111
16	88	14.2	390	4	US-09-543-681A-7837
17	85	13.7	348	4	US-09-252-991A-31249
18	85	13.7	416	4	US-09-540-236-2215
19	84.5	13.7	360	4	US-09-252-991A-23023
20	83.5	13.5	348	4	US-09-328-352-6843
21	83	13.4	411	4	US-09-489-039A-12676
22	79.5	12.8	351	1	US-08-319-387-6
23	78.5	12.7	524	4	US-09-252-991A-27006
24	77	12.4	425	4	US-09-252-991A-29530
25	76	12.3	139	4	US-09-252-991A-25783
26	76	12.3	403	4	US-09-252-991A-25706
27	76	12.3	424	4	US-09-252-991A-18548

28 75.5 12.2 91 4 US-09-198-452A-381 Sequence 381, Appl
29 74.5 12.0 114 4 US-09-540-236-3583 Sequence 3583, Ap
30 74 12.0 100 4 US-09-543-681A-4254 Sequence 4254, Ap
31 74 12.0 346 4 US-09-252-991A-24156 Sequence 24156, A
32 73.5 11.9 840 4 US-09-489-039A-11722 Sequence 11722, A
33 72 11.6 301 4 US-09-252-991A-28188 Sequence 28188, A
34 72 11.6 527 4 US-09-252-991A-32457 Sequence 32457, A
35 70.5 11.4 144 2 US-09-049-577-2 Sequence 2, Appli
36 70.5 11.4 144 3 US-09-390-598-2 Sequence 2, Appli
37 70.5 11.4 144 4 US-09-328-553-2 Sequence 2, Appli
38 70.5 11.4 172 4 US-09-252-991A-26259 Sequence 26259, A
39 70.5 11.4 582 4 US-09-516-914-21 Sequence 21, Appl
40 69 11.1 413 4 US-09-489-039A-13838 Sequence 13838, A
41 69 11.1 676 4 US-09-252-991A-23181 Sequence 23181, A
42 69 11.1 1333 4 US-09-347-878-20 Sequence 20, Appl
43 68.5 11.1 352 4 US-09-504-358-18 Sequence 18, Appl
44 68.5 11.1 352 4 US-09-954-314-18 Sequence 18, Appl
45 68 11.0 247 4 US-09-134-000C-5181 Sequence 5181, Ap

ALIGNMENTS

RESULT 1
US-09-453-956-8
; Sequence 8, Application US/09453956
; Patent No. 6472191
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya; No. 6472191oto, Tsuyoshi; Imamura, Takeshi;
; APPLICANT: Canon Kabushiki Kaisha
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
; TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
; TITLE OF INVENTION: Method for Degrading Halogenated Aliphatic Hydrocarbon
; TITLE OF INVENTION: Compounds and Aromatic Compounds, and
; TITLE OF INVENTION: Method for Environmental Remediation
; FILE REFERENCE: CFI0407AUS
; CURRENT APPLICATION NUMBER: US/09/453,956
; CURRENT FILING DATE: 1999-12-03
; EARLIER APPLICATION NUMBER: JP P1998-344506
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Ralstonia eutropha
; FEATURE:
; OTHER INFORMATION: TomQ polypeptide
US-09-453-956-8

Query Match 67.6%; Score 418.5; DB 4; Length 111;
Best Local Similarity 76.7%; Pred. No. 2e-42;
Matches 79; Conservative 9; Mismatches 12; Indels 3; Gaps 1;
QY 9 TWTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVKVRLRGAVRKLGPGR 69
Db 8 TVRVAQTGFSFGTAGESLLAGMAKLGRRGIPVGCINGCGVKVRLSGDVRKLGPVSR 67
QY 69 AHVSAEEENDGVALACRVVDDGVLEVAAGRLRKPFCGMACA 111
Db 68 AHVSADEELGTYTLACRVAPOGDVELEVAAGRMKPFPLC---CA 107

RESULT 2
US-09-716-865-2
; Sequence 2, Application US/09716865
; Patent No. 6548292
; GENERAL INFORMATION:
; APPLICANT: Bramuccci, Micheal G
; APPLICANT: Nagarajan, Vasantha
; APPLICANT: Chen, Mario W.
; TITLE OF INVENTION: Bacterial Plasmid Having Genes Encoding Enzymes for the
; TITLE OF INVENTION: Degradation of Aromatic Compounds

FILE REFERENCE: BC1016 US NA
 CURRENT APPLICATION NUMBER: US/09/716,865
 CURRENT FILING DATE: 2000-11-26
 PRIOR APPLICATION NUMBER: 60/167,062
 PRIOR FILING DATE: 1999-11-23
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 2
 LENGTH: 119
 TYPE: PRT
 ORGANISM: Pseudomonas CT14
 US-09-716-865-2

Query Match 52.0%; Score 322; DB 4; Length 119;
 Best Local Similarity 56.4%; Pred. No. 7e-31;
 Matches 62; Conservative 13; Mismatches 35; Indels 0; Gaps 0;
 Qy 9 TTTTAQTDERACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISR 68
 Db 10 SVHWQIGETPCATDESLLQGLRLGRKGIPVGVNGGCGVCKVHVIEGQCRPLGPVSR 69
 Qy 69 AHVSAEENDGYALACRVVDPDVELEVAGRLRPFPGCMACGTAINK 118
 Db 70 AHVSAEAEARGFTLACRVAPVTPVQLEVVGKFEKVFSGFVSTNEIINK 119

RESULT 3
 US-08-499-215-5
 Sequence 5, Application US/08499215
 Patent No. 5612204
 GENERAL INFORMATION:
 APPLICANT: Saeki, Hisashi
 APPLICANT: Miura, Akira
 TITLE OF INVENTION: BIOLOGICAL DEGRADATIVE
 TITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
 STREET: 2100 Pennsylvania Avenue
 CITY: N.W.
 STATE: Washington D.C.
 COUNTRY: U.S.A.
 ZIP: 20037-3202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 SOFTWARE: & WordPerfect version 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/499,215
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP Hei-6-179689
 FILING DATE: 08-JUL-1994
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 342 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-499-215-5

Query Match 23.3%; Score 144.5; DB 1; Length 342;
 Best Local Similarity 38.6%; Pred. No. 4.1e-09;
 Matches 39; Conservative 13; Mismatches 44; Indels 5; Gaps 4;
 Qy 9 TTTTAQTDERACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISR 68
 Db 3 TINVPFHSYSCDEGSLLDG-ALRNSLLIKYCKGGCGTCKVRLDGDVPEPGS-SF 60
 Qy 69 AHVSAEENDGYALACRVVDPDVELEVAGRLRPFPGCMACGTAINK 119

Db 61 ALTPEDREND-VILACASVPLEPCTIDVPSGLTEEEFFSG 100

RESULT 4
 US-09-252-991A-17118
 Sequence 17118, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 17118
 LENGTH: 391
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-17118

Query Match 18.3%; Score 113; DB 4; Length 391;
 Best Local Similarity 37.3%; Pred. No. 2.8e-05;
 Matches 28; Conservative 12; Mismatches 25; Indels 10; Gaps 3;
 Qy 24 GESLLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISR-VAEENNDGY 80
 Db 323 GETVHAANAALGLH-IPKACGCGICGTCV-----MKTAGEVMEHNGGITDDEVAEGY 375
 Qy 81 ALACRVVDPDVELEV 95
 Db 376 ILSCCVKPKGVDVID 390

RESULT 5
 US-09-489-039A-14027
 Sequence 14027, Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 14027
 LENGTH: 387
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-14027

Query Match 17.9%; Score 111; DB 4; Length 387;
 Best Local Similarity 35.8%; Pred. No. 4.7e-05;
 Matches 34; Conservative 13; Mismatches 40; Indels 8; Gaps 5;
 Qy 9 TTTTAQTD-ERYACVSGE--SLLAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGP 65
 Db 294 TTTTQGRDRLIALSADDDSLDAAURQG-ADLPFACKGVGVCATCKVLRGEVMAAN 352
 Qy 66 ISRAHVSAAEENDGYALACRVVDPDVELEVAGRLRPFPGCMACGTAINK 118
 Db 353 YS---LEADELAAGVILSCQSLPTSGDVVVDVDAR 384

RESULT 6

```

US-08-737-825-7
; Sequence 7, Application US/08737825
; Patent No. 5871922
; GENERAL INFORMATION:
; APPLICANT: SALMOND, GEORGE PEACOCK COPELAND
; APPLICANT: MCGOWAN, SIMON JAMES
; APPLICANT: SEBAIHA, MOHAMMED
; APPLICANT: COX, ANTHONY RICHARD JOHN
; APPLICANT: HOLDEN, MATTHEW THOMAS GEOFFREY
; APPLICANT: PORTER, LAUREN ELIZABETH
; APPLICANT: BYCROFT, BARRIE WALSHAM
; APPLICANT: WILLIAMS, PAUL
; APPLICANT: STEWART, GORDON SIDNEY ANDERSON BIRNIE
; TITLE OF INVENTION: GENES INVOLVED IN THE BIOSYNTHETIC PATHWAY OF CARBAPENEM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,825
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1009-0105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Erwinia carotovora

US-08-737-825-7
Query Match 17.8%; Score 110; DB 2; Length 92;
Best Local Similarity 39.7%; Pred. No. 1e-05;
Matches 29; Conservative 11; Mismatches 25; Indels 8; Gaps 3;

QY 25 ESSLAGMAKLRGIPVGCINGCGVKVRLGAVR--KLGPISSRAHVSAAEENDGYAL 82
Db 21 ESVLSAYEAGVE-LPYRCASGYCGVKRLTSGNVNMDHSGISRKIDIA-----DGYIL 74

QY 83 ACRVVPDGDVLE 95
Db 75 PCCSVPLSNLEIE 87

RESULT 7
5171684-7
; Patent No. 5171684
; APPLICANT: YEN, KWANG-MUI BLATT, LAWRENCE M.; KARL, MICHAEL R.
; TITLE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE
; MONOOXYGENASE OF PSEUDOMANAS MENDOCINA KR-1
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/590,374

```

```

; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 177,631
; FILING DATE: 05-APR-1988
; SEQ ID NO: 7:
; LENGTH: 326
; 5171684-7

Query Match 16.9%; Score 104.5; DB 6; Length 326;
Best Local Similarity 31.5%; Pred. No. 0.00023;
Matches 28; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

QY 14 QTDE---RYACVSGESLLAGMAKLRGRRGIPVGCINGCGVKVRLGAVRKLGPISSRAH 70
Db 5 QSDDLLHFEADSNDTLLSA-ALRAELVFFYECNCGCGACKTELLEGEVSNLWP-DAPG 62

QY 71 VSAEEENDGYALACRVVPDGDVELEVAGR 99
Db 63 LAARELKNRFLACQCKPLSLDKIKVINR 91

RESULT 8
US-09-543-681A-7190
; Sequence 7190, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709,1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7190
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7190

Query Match 16.6%; Score 103; DB 4; Length 353;
Best Local Similarity 34.1%; Pred. No. 0.00038;
Matches 30; Conservative 13; Mismatches 37; Indels 8; Gaps 3;

QY 9 TVTIAQTDERYACVSGESLLAGMAKLRGRRGIPV--GCLNGCGVKVRLGAVRKLGPI 66
Db 271 TWTIRHPLKQINVPVGMWILLTAMEE---NSVPVLAACRAGVCGSCKTRIVKGDYE---VT 324

QY 67 SRAHVSAAEENDGYALACRVVPDGDVLE 94
Db 325 STSTLTADBIAGQYVLACSCRLTGDVLE 352

RESULT 9
US-09-328-352-6375
; Sequence 6375, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6375
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6375

Query Match 15.5%; Score 96; DB 4; Length 358;

```

Best Local Similarity 30.9%; Pred. No. 0.0026;
Matches 25; Conservative 12; Mismatches 32; Indels 12; Gaps 3;

Qy 10 VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRLRGAVRKLGPISRA 69

Db 281 VSVAQDD-----ESILDAALRAG-ADLFYACKGGVCAFCRCKVLSGEYDMFLNYS-- 329

Qy 70 HVSAAEENDGYALACRVVDPG 90

Db 330 -LEEDEVEKGYVLSQTLIPKG 349

RESULT 10

US-09-543-681A-5480

; Sequence 5480, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543.681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 5480

; LENGTH: 411

; TYPE: PRT

; ORGANISM: Proteus mirabilis

US-09-543-681A-5480

Query Match

Best Local Similarity 15.3%; Score 94.5; DB 4; Length 411;

Matches 27; Conservative 17; Mismatches 33; Indels 7; Gaps 4;

Qy 16 DERYACVSGESLLAGMAKLGRRGIPV--GCLNGG-CGVCKVRLRGAVRKLGPISRAHVS 72

Db 47 EKSFPAGDKLL--NVLSNEGIFISSACGGGCGQCKVKVLEGGGDIL-PTLSHIN 102

Qy 73 ABEENDGYALACRVVDPGDVELEV 96

Db 103 KREAKEGCRACQNVKNKXLEL 126

RESULT 11

US-09-489-039A-12074

; Sequence 12074, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489.039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 12074

; LENGTH: 339

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-12074

Query Match

Best Local Similarity 14.9%; Score 92.5; DB 4; Length 339;

Matches 28; Conservative 10; Mismatches 35; Indels 5; Gaps 3;

Qy 17 BRYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRLRGAVRKLGPISRAHVSAREE 76

Db 266 EBYAPV-GTLLLDAL-ESNKVPTVACRAGVCGGCKTKVSG---KYSVTSTMTLTDAL 320

Qy 77 NDGYALACRVVDPGDVEL 94

Db 321 ADGVVLACSCHPQSDLVL 338

RESULT 12

US-09-489-039A-9429

; Sequence 9429, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489.039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 9429

; LENGTH: 377

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-9429

Query Match

Best Local Similarity 14.7%; Score 91; DB 4; Length 377;

Matches 27; Conservative 17; Mismatches 43; Indels 4; Gaps 3;

Qy 9 TTTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVCKVRLRGAVRKLGPIS 67

Db 290 TITLASTGERWP-VPGDKTIAQVLQEHGVAVPLSCMGICGACLTTPVREGTVDRHTVQS 348

Qy 68 RAHVSAREENDGYALACRVVDPGDVELEVAG 98

Db 349 EAEQAAEQH--IALCCRSLSANLIVIDLAG 377

RESULT 13

US-09-198-452A-952

; Sequence 952, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griflais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198.452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 952

; LENGTH: 431

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-952

Query Match

Best Local Similarity 14.6%; Score 90.5; DB 4; Length 431;

Matches 26; Conservative 14; Mismatches 33; Indels 7; Gaps 3;

Qy 23 SGESLLAGMAKLGRRGIPVGCINGG---CGVCKVRLRGAVRKLGPISRAHVSARENDG 79

Db 57 SGQTLVLSLLS---SGIPSPCGGKATCKQCKVRVKNNADEPL-ETDRSTFSKRLREG 112

Qy 80 YALACRVVDPGDVELEVAGR 99

Db 113 WRLSCQCKVQHDMSLEIEER 132

RESULT 14

US-09-453-956-7

; Sequence 7, Application US/09453956

```

; Patent No. 6472191
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya; No. 6472191oto, Tsuyoshi; Imamura, Takeshi;
; APPLICANT: Canon Kabushiki Kaisha
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
; TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
; TITLE OF INVENTION: Method for Degrading Halogenated Aliphatic Hydrocarbon
; TITLE OF INVENTION: Compounds and Aromatic Compounds, and
; TITLE OF INVENTION: Method for Environmental Remediation
; FILE REFERENCE: CP014074US
; CURRENT APPLICATION NUMBER: US/09/453,956
; CURRENT FILING DATE: 1999-12-03
; EARLIER APPLICATION NUMBER: JP P1998-344506
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Ralstonia eutropha
; FEATURE:
; OTHER INFORMATION: Tomp polypeptide
US-09-453-956-7

```

```

Query Match      14.2%; Score 88; DB 4; Length 352;
Best Local Similarity 34.7%; Pred. No. 0.023;
Matches 25; Conservative 9; Mismatches 36; Indels 2; Gaps 2;

QY 24 GESILAGMAKLRGIPVGLGCGVCKVRLRGAVRKLGPISRAHVSAAEENDGYALA 83
   |:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 19 GQTILDAALRGYI-IPHACCHGLCGTCKVSLDGEA-DLGEANPFALMDFEREKGALA 76
   |:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 84 CRVVPDGDVELE 95
   | | | | |
Db 77 CCATLQADTTIE 88

```

```

RESULT 15
US-09-489-039A-12111
; Sequence 12111, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12111
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12111

```

```

Query Match      14.2%; Score 88; DB 4; Length 381;
Best Local Similarity 31.2%; Pred. No. 0.026;
Matches 25; Conservative 14; Mismatches 33; Indels 8; Gaps 3;

QY 9 TVTIAQTDERYACVSGESILAGMAKLRGIPVGLGCGVCKVRLRGAVRKLGPISR 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 302 TVAIWQGGQFTNNQOVLELEQQGIR-VPYSCRAGICGSCRIRLEGEV---SPLKK 357
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 69 AHVSAEEENDGYALACRVVP 88
   | | | | | | | | | |
Db 358 NAVA-----GDGTLACSCVP 373

```

Search completed: August 5, 2004, 13:09:54
Job time : 19 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 5, 2004, 13:08:34 ; Search time 46 Seconds
(without alignments)
804.665 Million cell updates/sec

Title: US-09-430-029-8

Perfect score: 619

Sequence: 1 MDAGRVCVGTITAOQDERYA.....RLKPFPCGMACGTAANK 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	619	100.0	118	9 US-09-430-029-8	Sequence 8, Appli
2	418.5	67.6	111	14 US-10-223-371B-8	Sequence 8, Appli
3	130.5	21.1	343	12 US-10-282-122A-50674	Sequence 50674, A
4	126.5	20.4	343	12 US-10-282-122A-49233	Sequence 49233, A
5	124.5	20.1	343	12 US-10-282-122A-47765	Sequence 47765, A
6	123	19.9	346	14 US-10-213-878-12	Sequence 12, Appl
7	123	19.9	346	14 US-10-213-878-12	Sequence 12, Appl
8	123	19.9	346	14 US-10-214-059-22	Sequence 22, Appl
9	123	19.9	346	14 US-10-214-059-22	Sequence 22, Appl
10	120	19.4	366	12 US-10-282-122A-69513	Sequence 69513, A
11	117	18.9	368	12 US-10-282-122A-67992	Sequence 67992, A
12	113	18.3	366	12 US-10-282-122A-66835	Sequence 66835, A
13	109.5	17.7	336	12 US-10-282-122A-65277	Sequence 65277, A
14	109	17.6	348	12 US-10-282-122A-50897	Sequence 50897, A
15	105.5	17.0	169	12 US-10-424-599-275773	Sequence 275773,

16	105	17.0	350	14 US-10-213-878-18	Sequence 18, Appl
17	105	17.0	350	14 US-10-214-059-18	Sequence 18, Appl
18	103.5	16.7	186	12 US-10-425-114-47415	Sequence 47415, A
19	103.5	16.7	512	9 US-09-738-626-6142	Sequence 6142, Ap
20	103	16.6	334	12 US-10-282-122A-68779	Sequence 68779, A
21	103	16.6	419	12 US-10-282-122A-49831	Sequence 49831, A
22	101.5	16.4	336	12 US-10-282-122A-65947	Sequence 65947, A
23	101	16.3	664	12 US-10-282-122A-53556	Sequence 53556, A
24	100	16.2	382	12 US-10-282-122A-48031	Sequence 48031, A
25	99	16.0	340	12 US-10-282-122A-77980	Sequence 77980, A
26	94.5	15.3	354	14 US-10-156-761-11884	Sequence 11884, A
27	92.5	14.9	322	12 US-10-282-122A-59569	Sequence 59569, A
28	92.5	14.9	345	12 US-10-282-122A-49127	Sequence 49127, A
29	91.5	14.8	323	12 US-10-282-122A-75961	Sequence 75961, A
30	90.5	14.6	431	12 US-10-282-122A-54966	Sequence 54966, A
31	90.5	14.6	431	15 US-10-289-762-952	Sequence 952, App
32	90	14.5	381	12 US-10-282-122A-50665	Sequence 50665, A
33	89.5	14.5	322	12 US-10-282-122A-42942	Sequence 42942, A
34	89	14.4	145	12 US-10-424-599-150076	Sequence 150076,
35	88	14.2	352	14 US-10-223-371B-7	Sequence 7, Appli
36	87	14.1	322	12 US-10-282-122A-55785	Sequence 55785, A
37	86.5	14.0	431	12 US-10-282-122A-55074	Sequence 55074, A
38	84.5	13.7	83	16 US-10-437-963-133198	Sequence 133198,
39	84.5	13.7	322	12 US-10-282-122A-66811	Sequence 66811, A
40	82	13.2	322	12 US-10-282-122A-59345	Sequence 69345, A
41	81	13.1	354	9 US-09-430-029-7	Sequence 7, Appli
42	80.5	13.0	134	15 US-10-216-464-31	Sequence 31, Appl
43	79.5	12.8	338	12 US-10-282-122A-44836	Sequence 44836, A
44	78.5	12.7	152	12 US-10-425-114-66819	Sequence 66819, A
45	78.5	12.7	152	12 US-10-425-114-67176	Sequence 67176, A

ALIGNMENTS

RESULT 1

US-09-430-029-8
; Sequence 8, Application US/094300029
; Patent No. US20020168738A1

GENERAL INFORMATION:

; APPLICANT: Yano, Tetsuya; No. US20020168738A1oto, tsuyoshi; Imamura, Takeshi; Canon
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
; TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
; TITLE OF INVENTION: Method for Degrading Chlorinated Aliphatic Hydrocarbon
; TITLE OF INVENTION: Compounds and Aromatic Compounds, and
; TITLE OF INVENTION: Method for Environmental Remediation
; FILE REFERENCE: CF013982US
; CURRENT APPLICATION NUMBER: US/09/430,029
; CURRENT FILING DATE: 1999-10-29
; EARLIER APPLICATION NUMBER: JP P1998-310801
; EARLIER FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
; FEATURE:
; OTHER INFORMATION: TomQ polypeptide

US-09-430-029-8

Query Match 100.0%; Score 619; DB 9; Length 118;

Best Local Similarity 100.0%; Pred. No. 6.8e-64;

Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAGRVCVGTITAOQDERYACVSGSLLAGMAKLRGRGIPVGLNGCGCVKVRVLRGAV 60

Db 1 MDAGRVCVGTITAOQDERYACVSGSLLAGMAKLRGRGIPVGLNGCGCVKVRVLRGAV 60

QY 61 RLKLGPTISRAHSAEENDGYALACRVDPDGVLEVAGRLRKPFCGMACGTAANK 118

Db 61 RLKLGPTISRAHSAEENDGYALACRVDPDGVLEVAGRLRKPFCGMACGTAANK 118

```
RESULT 2
US-10-223-371B-8
; Sequence 8, Application US/10223371B
; Publication No. US20030170877A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Tetsuya; No. US20030170877A1oto, Tsuyoshi; Imamura, Takeshi; Canon
; APPLICANT: Kabushiki Kaisha
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene, Recombinant
; TITLE OF INVENTION: Plasmid, Transformed Microorganism, Method for Degrading Halogen
; TITLE OF INVENTION: Aliphatic Hydrocarbon Compounds and Aromatic Compounds, and Meth
; TITLE OF INVENTION: Environmental Remediation
; FILE REFERENCE: 03500.014074.1
; CURRENT APPLICATION NUMBER: US/10/223.371B
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US/09/453,956
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 8
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Ralstonia eutropha
; FEATURE:
; OTHER INFORMATION: TomQ polypeptide
US-10-223-371B-8

Query Match 67.6%; Score 418.5; DB 14; Length 111;
Best Local Similarity 76.7%; Pred. No. 1.2e-40;
Matches 79; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY 9 TTTAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVKVRVLRGAVRKLGPISR 68
DB 8 TVRVAQTGESFSCSTAGESLLAGMAKLGRRGIPVGCINGCGVKVRVLRGAVRKLGPISR 67

QY 69 AHVSAEEENDGYALACRVVPGDVELEVAGRLRKPFFCGMACA 111
DB 68 AHVSADEEGLYTLACRVAPQGDVELEVAGRWKQKFLC--CA 107

RESULT 3
US-10-282-122A-50674
; Sequence 50674, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/269,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 49233
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49233

Query Match
Best Local Similarity 20.4%; Score 126.5; DB 12; Length 343;
Matches 34; Conservative 15; Mismatches 34; Indels 13; Gaps 4;

QY 10 VTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVKVRLRGAVRKLGPISRA 69
Db 5 VTLKQSGRQFQVEDEPVLAAALRQVH-IPYCKNGAGCSCKGIVSGQIEQ-GPHAAS 62
QY 70 HVSAREENDGYALACRVVDPGDVDEL---EVAG 98
Db 63 ALSNDERTRGALLCCSKAQCDLEIDVREIAG 94

RESULT 6
US-10-213-878-12
; Sequence 12, Application US/10213878
; Publication No. US20030073206A1
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; APPLICANT: Nagarajan, Vasantha
; APPLICANT: Thomas, Stuart
; TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted
; FILE REFERENCE: CL1662 US NA
; CURRENT APPLICATION NUMBER: US/10/213,878
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/311,490
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Sphingomonas sp.
US-10-213-878-12

Query Match
Best Local Similarity 19.9%; Score 123; DB 14; Length 346;
Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;

QY 9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVKVRLRGAVRKLGPISR 68
Db 12 TVTVEGSPITLDIPAGKTLLEMLDAG-LAMPDHCKVSGCTCKFKLVSKIGELSPSAL 70
QY 69 AHVSAREENDGYALACRVVDPGDVDELVEVAGRLKPPFCGMACA 111
Db 71 A-LEGDELSRGLACQAIIPRDLTIAVDA---PLSQGIAIA 108

RESULT 7
US-10-213-878-22
; Sequence 22, Application US/10213878
; Publication No. US20030073206A1
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; APPLICANT: Nagarajan, Vasantha
; APPLICANT: Thomas, Stuart
; TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted
; FILE REFERENCE: CL1662 US NA
; CURRENT APPLICATION NUMBER: US/10/213,878
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/311,490
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Sphingomonas sp.
US-10-213-878-22

Query Match
Best Local Similarity 19.9%; Score 123; DB 14; Length 346;
Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;

QY 9 TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCINGCGVKVRLRGAVRKLGPISR 68
```



```
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67992
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-67992

Query Match      18.9%; Score 117; DB 12; Length 368;
Best Local Similarity 40.3%; Pred. No. 6.1e-05;
Matches 29; Conservative 10; Mismatches 29; Indels 4; Gaps 2;

QY 24 GESLLAGMAKLGRRGIPVGCINGCGVKVRVLRGAVRKLGPISRAHVSAAEENDGYALA 83
Db 300 GETVHAARAAKVLGLM-IPKACGMGICGTCVKVLKLGVEVEM---EHNNGITDEDEAGYILS 355
QY 84 CRVVPDGDVLE 95
Db 356 CCSVPKGDVRID 367

RESULT 12
US-10-282-122A-66835
; Sequence 66835, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John

; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John

; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67992
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66835

Query Match      18.3%; Score 113; DB 12; Length 366;
Best Local Similarity 37.3%; Pred. No. 0.00018;
Matches 28; Conservative 12; Mismatches 25; Indels 10; Gaps 3;

QY 24 GESLLAGMAKLGRRGIPVGCINGCGVKVRVLRGAVRKLGPISRAH---VSAEEENDGY 80
Db 298 GETVHAARAAKVLGLH-IPKACGMGICGTCVKV-----MKTAGEVEMEHNGITDEDAEGY 350
QY 81 ALACRVVPDGDVLE 95
Db 351 ILSCCSVPKGDVVVID 365

RESULT 13
US-10-282-122A-65277
; Sequence 65277, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
```

```

RESULT 14
US-10-282-122A-50897
; Sequence 50897, Application US/10282122A
; Publication No. US20040029129A1
;
GENERAL INFORMATION:
;
APPLICANT: Wang, Liangsu
;
APPLICANT: Zamudio, Carlos
;
APPLICANT: Malone, Cheryl
;
APPLICANT: Haselbeck, Robert
;
APPLICANT: Ohlsen, Kari
;
APPLICANT: Zyskind, Judith
;
APPLICANT: Wall, Daniel
;
APPLICANT: Trawick, John
;
APPLICANT: Carr, Grant
;
APPLICANT: Yamamoto, Robert
;
APPLICANT: Forsyth, R.
;
APPLICANT: Xu, H.
;
TITLE OF INVENTION: Identification of E
;
FILE REFERENCE: ELITRA.034A
;
CURRENT APPLICATION NUMBER: US/10/282,1
;
CURRENT FILING DATE: 2003-02-20
;
PRIOR FILING DATE: 2000-03-21
;
PRIOR APPLICATION NUMBER: 60/191,078
;
PRIOR FILING DATE: 2000-03-21
;
PRIOR APPLICATION NUMBER: 60/206,848
;
PRIOR FILING DATE: 2000-05-23
;
PRIOR APPLICATION NUMBER: 60/207,727
;
PRIOR FILING DATE: 2000-05-26
;
PRIOR APPLICATION NUMBER: 60/230,335
;
PRIOR FILING DATE: 2000-09-06
;
PRIOR APPLICATION NUMBER: 60/230,347
;
PRIOR FILING DATE: 2000-09-09
;
PRIOR APPLICATION NUMBER: 60/242,578
;
PRIOR FILING DATE: 2000-10-23
;
PRIOR APPLICATION NUMBER: 60/242,578
;
PRIOR FILING DATE: 2000-10-23
;

```

```
Query Match      17.0%; Score 105.5; DB 12; Length 169;
Best Local Similarity 40.0%; Pred. No. 0.0005;
Matches 24; Conservative 9; Mismatches 18; Indels 9; Gaps 2
QY 39 IPVGCLNGCGVKVRVLRGAVRK--LGPISRAHVSAEEENDGVALACRVVPDGDVELE 95
    :|::||::||::||:||||:||||:||||:|
Db 81 LPFACRHGGCTSCAARIKKGIQRPEALG-----ISAELRDKGVALICVGFFPTSDVEVE 134
```

Search completed: August 5, 2004, 13:14:34
Job time : 48 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 5, 2004, 13:13:39 ; Search time 16 Seconds
(without alignments)
709.413 Million cell updates/sec

Title: US-09-430-029-8
Perfect score: 619
Sequence: 1 MDAGRVCCTVIAQTDERYA.....RLRKPFFCGMACAGTAAINK 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_78:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195.5	31.6	112	1	S16193
2	186	30.0	108	1	B39181
3	172.5	27.9	93	2	T31266
4	172.5	27.9	112	1	S24417
5	166.5	26.9	101	1	S54762
6	129.5	20.9	329	2	T46585
7	123	19.9	346	2	T31263
8	114	18.4	337	2	A12723
9	114	18.4	337	2	E97505
10	113	18.3	366	2	G82970
11	112	18.1	411	1	D64052
12	106	17.1	353	2	A95312
13	105	17.0	350	2	B37316
14	104.5	16.9	326	1	A47016
15	104	16.8	405	2	D81918
16	104	16.8	405	2	G81184
17	102	16.5	369	2	AG0825
18	101.5	16.4	181	2	A86451
19	101.5	16.4	336	2	F81849
20	101	16.3	378	2	AF3320
21	100.5	16.2	348	1	JQ0701
22	99.5	16.1	122	2	S75687
23	99	16.0	340	2	A10165
24	99	16.0	408	2	B82094
25	99	16.0	685	2	C70878
26	98	15.8	353	1	S44308
27	98	15.8	353	2	F37831
28	98	15.8	354	2	C95381
29	98	15.8	407	1	S65531

ALIGNMENTS

RESULT 1

S16193 ferredoxin [2Fe-2S]-like protein xylT - Pseudomonas putida plasmid pW00

C:Species: Pseudomonas putida
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: S16193; S23486
R:Harayama, S.; Polissi, A.; Rekik, M.

FEBS Lett. 285, 85-88, 1991

A:Title: Divergent evolution of chloroplast-type ferredoxins.

A:Reference number: S16193; MUID:91293320; PMID:2065785

A:Accession: S16193

A:Molecule type: DNA

A:Residues: 1-112 <HAR>

A:Cross-references: EMBL:X61467; NID:g311898; PIDN:CAA43702.1; PID:g311899

R:Neidle, E.L.; Hartnett, C.; Orntson, L.N.; Bairoch, A.; Rekik, M.; Harayama, S.

Eur. J. Biochem. 204, 113-120, 1992

A:Title: Cis-diol dehydrogenases encoded by the TOL pW00 plasmid xylL gene and the Acine

A:Reference number: S23477; MUID:92155191; PMID:1740120

A:Accession: S23486

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-112 <NEI>

A:Cross-references: EMBL:M64747; NID:g151718; PIDN:AAA26051.1; PID:g151723

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1992

C:Genetics:

A:Gene: xylT

A:Genome: plasmid pW00

C:Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology

C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein

F;25-82/Domain: ferredoxin [2Fe-2S] homology <FER>

F;41,46,49,81/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 31.6%; Score 195.5; DB 1; Length 112;

Best Local Similarity 48.1%; Pred. No. 3.4e-12;

Matches 38; Conservative 13; Mismatches 27; Indels 1; Gaps 1;

QY 17 ERYACVSGSLLAGMAKLGRIPIVCLNGGCGVKRVLRGAVRKLGPISRAHVSAREE 76

Db 15 QSRFCAGCGSVLRAMEAQGRKCIPIVCGRGCGCLCRVRLSGAYRS-GRMSRGHVPAAKAA 73

QY 77 NDGYALACRWPDGDVELE 95

Db 74 AEALACQVFFQTDLTIE 92

RESULT 2

B39181

ferredoxin [2Fe-2S]-like protein nahG-nahH intergenic region - Pseudomonas putida (stra

C:Species: Pseudomonas putida

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: B39181; S16368

R:You, I.S.; Ghosal, D.; Gunsalus, I.C.

```

ferredoxin [2Fe-2S]-like protein dmpQ - Pseudomonas putida
Cs:species: Pseudomonas putida
C:date: 03-dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:accession: S24417
R:Shingler, V.; Powlowski, J.; Marklund, U.
J. Bacteriol. 174, 711-724, 1992

```

[illegible]

RESULT 6

T46585
ferredoxin reductase [imported] - Pseudomonas stutzeri
C:Species: Pseudomonas stutzeri
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 11-May-2000
C:Accession: T46585
R:Ouchiya, N.; Miyachi, S.; Omori, T.
J. Gen. Appl. Microbiol. 44, 57-63, 1998
A:Title: Cloning and nucleotide sequence of carbazole catabolic genes from Pseudomonas
A:Reference number: 223091
A:Accession: T46585
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-329 <OUC>
A:Cross-references: EMBL:AB001723; PIDN:BAA31273.1
A:Experimental source: strain OM1
C:Function:
C:Superfamily: methan monooxygenase reductase component; cytochrome-b5 reductase homolog

Query Match 20.9%; Score 129.5; DB 2; Length 329;
Best Local Similarity 39.0%; Pred. No. 2.9e-05;
Matches 30; Conservative 11; Mismatches 35; Indels 1; Gaps 1;

QY 21 CVSGESLLAGMAKLGRRGIPVGLNGCGVCKVRLRGAVRKLGPISRAHVSAEENDGY 80
DB 14 CDSGKSLVLSALANG-IGFFPYECASGGCGVCKFELLEGNVQSMWPDAPCLSSRDREKGNR 72

QY 81 ALACRVVPDGDVELEVA 97
DB 73 HLACQCVALSDLRIKVA 89

RESULT 7
T31263
xylene monooxygenase (EC 1.-.-.-) chain A - Sphingomonas aromaticivorans plasmid pNL1
C:Species: Sphingomonas aromaticivorans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T31263
R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; et al.
submitted to the EMBL Data Library, July 1998
A:Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromaticivorans
A:Reference number: 220992
A:Accession: T31263
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-346 <ROM>
A:Cross-references: EMBL:AF079317; NID:G3378261; PID:G3378404; PIDN:AAD03987.1
C:Genetics:
A:Gene: xyla
A:Genome: plasmid pNL1
C:Superfamily: methan monooxygenase reductase component; cytochrome-b5 reductase homolog
C:Keywords: oxidoreductase

Query Match 19.9%; Score 123; DB 2; Length 346;
Best Local Similarity 30.1%; Pred. No. 0.00013;
Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;

QY 9 TTTTAQTDERYACVSGESLLAGMAKLGRRGIPVGLNGCGVCKVRLRGAVRKLGPISR 68
DB 12 TVTVGSGPTTLDIPAGKTLLLEAMLDAG-LAMPDHCKVSGCGTCKFLVSGKIGELSPSAL 70

QY 69 AHVSAEENDGVALACRVVPDGDVELEVAAGRLRKPFFCGMACA 111
DB 71 A-LEGDELRSGLACQAIAPRSDLTIAVDA---PLSQGIAIA 108

RESULT 8
A12723
naphthalene 1,2-dioxygenase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: A12723
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 02-Aug-2002
C;Accession: G82970
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, L.; Lory, S.; Olson, M.V.
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G82970
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-366 <STO>
A;Cross-references: GB:AB004953; GB:AE004091; NID:G9951727; PIDN:AAG08796.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA5411
C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferredoxin
Query Match 18.3%; Score 113; DB 2; Length 366;
Best Local Similarity 37.3%; Pred. No. 0.0013;
Matches 28; Conservative 12; Mismatches 25; Indels 10; Gaps 3;
QY 24 GESILAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISRAH---VSAEENDGY 80
DB 298 GETVHAARAKLGLH-IPKACGNGICGTCKV-----MKTAGEVMEHGGITDEDVAREGY 350
QY 81 ALACRVVDPGDVELE 95
DB 351 ILSCCVKPGDVID 365
RESULT 11
D64052
Na+-translocating NADH-ubiquinone oxidoreductase (EC 1.-.-.-) beta chain - Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: D64052
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Drenth, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrman, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A;Reference number: A64000; MUID:195350630; PMID:7542800
A;Accession: D64052
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-411 <TIGR>
A;Cross-references: GB:U32702; GB:L42023; NID:G1573118; PIDN:AAC21841.1; PID:G1573127; TIGR:1573127
C;Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homology
C;Keywords: 2Fe-2S; flavoprotein; iron-sulfur protein; metalloprotein; oxidoreductase
F;58-115/Domain: ferredoxin [2Fe-2S] homology <FER>
F;140-409/Domain: cytochrome-b5 reductase homology <CBR>
F;73,79,82,114/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
Query Match 18.1%; Score 112; DB 1; Length 411;
Best Local Similarity 34.7%; Pred. No. 0.0019;
Matches 33; Conservative 16; Mismatches 36; Indels 10; Gaps 5;
QY 8 GTVTIAQTDERVACV---SGESILAGMAKLGRRGIPV---GCLNGG-CGVCKVRVLRGAVR 61
DB 36 GDITIDNDPEKATLTPAGKLLGALAS---KGIFVSSACGGGCGCQIVKVGNGGE 92
QY 62 KLGPISRAHVSABEENDGYALACRVVDPGDVELEV 96
DB 93 IL-PTLSHINKREAGEVRLAQQVNVKGNMEVEL 126
RESULT 12
A95312
probable dioxygenase reductase subunit [imported] - *Sinorhizobium meliloti* (strain 1021)
C;Species: *Sinorhizobium meliloti*
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: A95312
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowler, S.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti* genome
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: A95312
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-353 <KUR>
A;Cross-references: GB:AE006469; PIDN:AAK65059.1; PID:G14523492; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, H.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; Yeh, K. A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*. A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMA0752
A;Genome: plasmid
Query Match 17.1%; Score 106; DB 2; Length 353;
Best Local Similarity 37.3%; Pred. No. 0.0063;
Matches 28; Conservative 8; Mismatches 35; Indels 4; Gaps 2;
QY 21 CVSGESILAGMAKLGRRGIPVGCINGCGVCKVRVLRGAVRKLGPISRAHVSABEENDGY 80
DB 282 CSETDTILAA-AKAGLVIPSGCSMGICGTCKVRKTGQVHM---VHNGGITDEDVEDGY 337
QY 81 ALACRVVDPGDVELE 95
DB 338 ILACCSKPLRRVSVE 352
RESULT 13
B37316
ferredoxin-NAD reductase (EC 1.18.1.3) chain A - *Pseudomonas putida* plasmid pWMO
N;Contains: ferredoxin-NAD+ reductase (EC 1.18.1.3)
C;Species: *Pseudomonas putida*
C;Date: 01-Oct-1992 #sequence_revision 01-Oct-1992 #text_change 03-Jun-2002
C;Accession: B37316; S29273
R;Suzuki, M.; Hayakawa, T.; Shaw, J.P.; Reikik, M.; Harayama, S. J. Bacteriol. 173, 1690-1695, 1991
A;Title: Primary structure of xylene monooxygenase: similarities to and differences from ferredoxin-NAD+ reductase
A;Reference number: A37316; MUID:91154124; PMID:1999188
A;Accession: B37316
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-350 <SUZ>
A;Cross-references: GB:M37480; NID:G151649; PIDN:AAA26027.1; PID:G151651
R;Shaw, J.P.; Harayama, S. Eur. J. Biochem. 209, 51-61, 1992
A;Title: Purification and characterization of the NADH: acceptor reductase component of ferredoxin-NAD+ reductase
A;Reference number: S29273; MUID:93011166; PMID:1327782
A;Accession: S29273
A;Molecule type: protein
A;Residues: 6-8,'X',10-12,'X',14-16 <SHA>
C;Genetics:
A;Gene: xyla
A;Genome: plasmid pWMO
C;Complex: heterodimer; chain A and chain M
C;Function:
A;Description: catalyzes hydroxylation of a methyl side-chain of toluene and xylenes;
C;Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homology
C;Keywords: 2Fe-2S; aromatic hydrocarbon catabolism; FAD; flavoprotein; heterodimer; 1Fe-2S; 2Fe-2S; ferredoxin [2Fe-2S] homology <FER>
F;37-93/Domain: ferredoxin [2Fe-2S] homology <FER>
F;121-344/Domain: cytochrome-b5 reductase homology <CBR>
F;52,57,60,92/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 17.0%; Score 105; DB 2; Length 350;
Best Local Similarity 28.4%; Pred. No. 0.0078;
Matches 25; Conservative 18; Mismatches 43; Indels 2; Gaps 2;
QY 9 TTVTIAQTDERVACVSGESLLAGMAKLGRRGIPVGLNGCGVCKVRVLRGAVRKLGPISR 68
Db 19 TVSVRGQGFQFKVPRGQTILESALHGG-IAFPHDCKVSGCGTKYKLIISGRNEL-TSSA 76
QY 69 AHVSAEEENDGYALACRVVPGDVLEV 96
Db 77 MGLSGDLYQSGYRLGQCQIPKEDLEIEL 104

RESULT 14
A47016
toluene-4-monooxygenase (EC 1.-.-.-) reductase component - Pseudomonas mendocina
C:Species: Pseudomonas mendocina
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A47016
R:Yen, K.M.; Karl, M.R.
J. Bacteriol. 174, 7253-7261, 1992
A:Title: Identification of a new gene, tmoF, in the Pseudomonas mendocina KRI gene cluster
A:Reference number: A47016; MUID:93054339; PMID:1429451
A:Accession: A47016
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-326 <YEN>
A:Cross-references: GB:M95045; NID:gl51596; PIDN:AAA26004.1; PID:gl51597
A:Experimental source: KRI
A:Note: sequence extracted from NCBI backbone (NCBIN:118027, NCBIP:118029)
C:Genetics:
A:Gene: tmoF
C:Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homol
C:Keywords: 2Fe-2S; flavoprotein; iron-sulfur protein; metalloprotein; oxidoreductase
F:21-77/Domain: ferredoxin [2Fe-2S] homology <FER>
F:107-320/Domain: cytochrome-b5 reductase homology <CBR>
F:36,41,44,76/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 16.9%; Score 104.5; DB 1; Length 326;
Best Local Similarity 31.5%; Pred. No. 0.0082;
Matches 28; Conservative 16; Mismatches 40; Indels 5; Gaps 3;
QY 14 QTDE---RYACVSGESLLAGMAKLGRRGIPVGLNGCGVCKVRVLRGAVRKLGPISRAH 70
Db 5 QSDDLLHFFEADNDTLISA-ALRAELVFPYCNSGGCGACKIELLEGEVSNLWP-DAPG 62
QY 71 VSAEEENDGYALACRVVPGDVLEVAGR 99
Db 63 LAARELKNRFLACQCKPLSLKIKVINR 91

RESULT 15
D81918
sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) chain F NMA0747 [simil
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: D81918
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: D81918
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <PAR>
A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84030.1; PID:g737946
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: nqrF; NMA0747
C:Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homol
C:Keywords: NAD; oxidoreductase

Query Match 16.8%; Score 104; DB 2; Length 405;
Best Local Similarity 35.2%; Pred. No. 0.011;
Matches 32; Conservative 14; Mismatches 41; Indels 4; Gaps 4;
QY 8 GTVTIAQTDERVACV-SGESLLAGMAKLGRRGIPVGLNGG-CGVCKVRVLRGAVRKLGP 65
Db 32 GDITIKVNGEKELTMPAGGKLIGALANEG-IFIPSA CGGGSCGCRVVVKSGGDIL-P 89
QY 66 ISRAHVSAAEEENDGYALACRVVPGDVLEV 96
Db 90 TELSHISKREAREGCRUSCQNVKTDMDIEV 120

Search completed: August 5, 2004, 13:17:20
Job time : 17 secs

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	195.5	31.6	112	1	PERF_PSEPU	P23103 pseudomonas
2	186	30.0	108	1	PERF_PSEPU	P23263 pseudomonas
3	112	18.1	411	1	NQRF_HAEIN	O05012 haemophilus
4	105	17.0	350	1	Xyla_PSEPU	P21394 pseudomonas
5	104.5	16.9	326	1	TMOF_PSEME	Q03304 pseudomonas
6	104	16.8	405	1	NQRF_NEIMA	Q9jvg3 neisseria m
7	104	16.8	405	1	NQRF_NEIMB	Q9k0m8 neisseria m
8	100.5	16.2	348	1	MMOC_METCA	P22868 methylococcus
9	99	16.2	407	1	NQRF_PASMU	Q9c1a6 pasteurella
10	99	16.0	408	1	NQRF_VIBCH	Q9x4q8 vibrio chol
11	98	15.8	352	1	DMPF_PSESP	P19734 pseudomonas
12	98	15.8	407	1	NQRF_VIBAL	Q56584 v na (+)-tra
13	96	15.5	407	1	NQRF_VIBPA	Q9lcj0 vibrio para
14	96	15.5	407	1	NQRF_VIBVU	Q8dbj1 vibrio vuln
15	93	15.0	407	1	NQRF_VERPE	Q8zbz5 yersinia pe
16	92.5	14.9	301	1	NQRF_SHEPU	Q9ic17 shewanella
17	92	14.9	93	1	PERF_PERRI	P10770 peridinium
18	91	14.7	104	1	FER2_SYNP6	P08451 synechococc
19	90.5	14.6	95	1	FER_GLEJA	P00233 gleichenia
20	90.5	14.6	356	1	PAAE_ECOLI	P76081 escherichia
21	90.5	14.6	431	1	NQRF_CHLNP	Q9-723 chlamydia p
22	90	14.5	407	1	NQRF_VIBHA	Q9xfv6 vibrio harv
23	89.5	14.5	96	1	FER1_PHYM	P00229 phytoacca
24	89.5	14.5	96	1	FER1_PHYES	P00230 phytolacca
25	89.5	14.5	303	1	NQRF_COLMA	Q9k3e1 colwellia m
26	89.5	14.5	303	1	NQRF_VIBBS	Q9lcj2 vibrio psyc
27	89.5	14.5	322	1	HCR_ECOLI	P75824 escherichia
28	88.5	14.3	431	1	NQRF_CHLTR	Q84745 chlamydia t
29	88	14.2	328	1	NDOR_PSEPU	Q52126 pseudomonas
30	87.5	14.1	348	1	BENC_ACICA	P07771 acinetobact
31	87	14.1	93	1	FER2_EQUITE	P00236 equisetum t
32	86.5	14.0	431	1	NQRF_CHLMU	Q9pli3 chlamydia m
33	86	13.9	93	1	FER2_EQUAR	P00237 emuisetum m


```

DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR PRINTS; PR00371; FENCR.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; FALSE_NEG.
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 5 27 POTENTIAL.
FT DOMAIN 38 120 FERREDOXIN.
FT DOMAIN 276 393 CATALYTIC.
FT METAL 73 73 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 79 79 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 82 82 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 114 114 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 411 AA; 45705 MW; E5560053E66D23E0 CRC64;

Query Match 18.1%; Score 112; DB 1; Length 411;
Best Local Similarity 34.7%; Pred. No. 0.00064;
Matches 33; Conservative 16; Mismatches 36; Indels 10; Gaps 5;

QY 8 GTVTIAOTDERYACV---SGESLIAGMAKLGRRGIPV--GCLNGG-GGVCKVRVLRGAVR 61
Db 36 GDIIDINDPEKAITLPAGKLLGALAS---KGIFVSSACGGGSCGQCIVKVGKGGE 92
QY 62 KLGPISRAHVSABEENDGYALACRVDPGDVELEV 96
Db 93 IL-PTLESHINKREKGYRLACQVNVKGNVEVL 126

RESULT 4
XYLA_PSEPU STANDARD; PRT; 350 AA.
AC P21394;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Xylene monooxygenase electron transfer component [Includes:
DE Ferredoxin; Ferredoxin-NAD(+) reductase (EC 1.18.1.3)].
GN XYLA.
OS Pseudomonas putida.
OG Plasmid TOL pMW0.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 6-16.
RX MEDLINE=91154124; PubMed=199388;
RA Suzuki M., Hayakawa T., Shaw J.P., Reik M., Hayayama S.;
RT "Primary structure of xylene monooxygenase: similarities to and
RT differences from the alkane hydroxylation system.";
RL J. Bacteriol. 173:1690-1695 (1991).
CC -!- FUNCTION: OXIDIZES TOLUENE AND XYLENES TO (METHYL)BENZYL
CC ALCOHOLS. THE ENZYME HAS A BROAD SPECIFICITY AND ALSO OXIDIZES
CC (METHYL)BENZYL ALCOHOLS TO (METHYL)BENZALDEHYDES AND INDOLE TO
CC INDOXYL.
CC -!- CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(+) = oxidized
CC ferredoxin + NADH.
CC -!- COFACTOR: FAD.
CC -!- SUBUNIT: COMPOSED OF TWO SUBUNITS: XYLA AND XYLM.
CC -!- SIMILARITY: IN THE N-TERMINAL REGION WITH 2FE-2S FERREDOXINS, AND
CC IN THE REST OF THE SEQUENCE WITH FERREDOXIN REDUCTASE.
CC -!- SIMILARITY: TO OTHER BACTERIAL RING-HYDROXYLATING DIOXYGENASE
CC ELECTRON TRANSFER COMPONENTS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----

```

```

DR EMBL; M37480; ABA26027.1; -.
DR EMBL; D63341; BAA09663.1; -.
DR PIR; B37316; B37316.
DR HSSP; P06543; 1CZP.
DR InterPro; IPR006058; 2Fe2S_fd_BS.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR008333; FAD_binding_6.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR InterPro; IPR001221; Phe_hydroxylase.
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00371; FENCR.
DR PRINTS; PR00410; PHEHYDRXLASE.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
KW Aromatic hydrocarbons catabolism; Flavoprotein; Oxidoreductase; FAD;
KW NAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S; Plasmid.
FT DOMAIN 41 108 FERREDOXIN
FT METAL 109 350 FERREDOXIN-NADH REDUCTASE.
FT METAL 52 52 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 57 57 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 60 60 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 92 92 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 350 AA; 38455 MW; 26828AC2226C1DDD CRC64;

Query Match 17.0%; Score 105; DB 1; Length 350;
Best Local Similarity 28.4%; Pred. No. 0.0027;
Matches 25; Conservative 18; Mismatches 43; Indels 2; Gaps 2;

QY 9 TVTIAOTDERYACVSGESLIAGMAKLGRRGIPVGCINGCGGVCKVRVLRGAVRKLGPISR 68
Db 19 TVSVRGQGFQKVPKRGQTLLESALHQG-IAPPHCKVKGSCGCKYKLISRVNEL-TSSA 76
QY 69 AHVSAEENDGYALACRVDPGDVELEV 96
Db 77 MGLSGDLYQSGYRLGCGQCPKEDLETEL 104

RESULT 5
TMOF_PSEME STANDARD; PRT; 326 AA.
AC Q03304;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Toluene-4-monooxygenase electron transfer component [Includes:
DE Ferredoxin; Ferredoxin-NAD(+) reductase (EC 1.18.1.3)].
GN TMOF.
OS Pseudomonas mendocina.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=300;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-14.
RC STRAIN=KRI.
RX MEDLINE=93054339; PubMed=1429451;
RA Yen K.-M., Karl M.R.;
RT "Identification of a new gene, tmoF, in the Pseudomonas mendocina KRI
RT gene cluster encoding toluene-4-monooxygenase.";
RL J. Bacteriol. 174:7253-7261 (1992).
CC -!- FUNCTION: ELECTRON TRANSFER COMPONENT OF TOLUENE 4-MONOOXYGENASE
CC COMPLEX.
CC -!- CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(+) = oxidized
CC ferredoxin + NADH.
CC -!- COFACTOR: FAD.
CC -!- PATHWAY: Toluene degradation; first step.
CC -!- SUBUNIT: THE MULTICOMPONENT ENZYME TOLUENE-4-MONOOXYGENASE
CC IS FORMED BY THE TMOA, TMOB, TMOG, TMOD, TMOE AND TMOF
CC POLYPEPTIDES.
CC -!- SIMILARITY: IN THE N-TERMINAL REGION WITH 2FE-2S FERREDOXINS, AND

```

IN THE REST OF THE SEQUENCE WITH FERREDOXIN REDUCTASE.

-1- SIMILARITY: TO OTHER BACTERIAL RING-HYDROXYLATING DIOXYGENASE ELECTRON TRANSFER COMPONENTS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

EMBL; M95045; AAA26004.1; --

PIR; A47016; A47016.

InterPro; IPR006058; 2Fe2S fd BS.

InterPro; IPR008333; FAD binding_6.

InterPro; IPR001041; Ferredoxin_.

InterPro; IPR001709; FPN cyt_redtse.

InterPro; IPR001433; Oxred_FAD/NAD(P).

InterPro; IPR001221; Phe hydroxylase.

Pfam; PF00970; FAD binding_6; 1.

Pfam; PF00111; fer2; 1.

Pfam; PF00175; NAD binding_1; 1.

PRINTS; PR00371; FENCR.

PRINTS; PR00410; PHEHYDRLASE.

PROSITE; PS00197; 2FE2S FERREDOXIN; 1.

KW Aromatic hydrocarbons catabolism; Flavoprotein; FAD; NAD; Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.

FT DOMAIN 25 94 FERREDOXIN.

FT DOMAIN 95 326

FT METAL 36 36 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 44 44 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

SQ SEQUENCE 326 AA; 35983 MW; 17889D794PC092EE CRC64;

Query Match 16.9%; Score 104.5; DB 1; Length 326;

Best Local Similarity 31.5%; Pred. No. 0.0029;

Matches 28; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

QY 14 QTDE--RVACVSGESLLAGMAKLGRRGIPVGLNGGCVKVRVLRGAVRKLGPISRAH 70

Db 5 QSDLLHHEAFDSNLTLLSA-ALRAELVFPYCNSGGCGACKIELLEGEVSNLWP-DAPG 62

QY 71 VSAEENDGYALACRVDPDGDVELEVAGR 99

Db 63 LAARELKNRFLACCKPLSLDKIKVINR 91

RESULT 6

NORF_NEIMA

ID NORF_NEIMA STANDARD; PRT; 405 AA.

AC Q9JYQ3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)

DE (Na(+)-translocating NOR subunit F) (Na(+)-NOR subunit F) (NOR complex subunit F) (NOR-1 subunit F).

GN NORF OR NMA0747.

OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI_TaxID=65699;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Z2491 / Serogroup A / Serotype 4A;

RA MEDLINE=20222556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491";

Nature 404:502-506(2000).

-1- FUNCTION: NOR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubiquinol by a one-electron transfer pathway (By similarity).

-1- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) + ubiquinol + Na(+) (Out).

-1- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).

-1- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE and nqrF (By similarity).

-1- SUBCELLULAR LOCATION: Inner membrane (Potential).

-1- SIMILARITY: Belongs to the nqrF family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

EMBL; AL162754; CAB84030.1; --

PIR; D81918; D81918.

HSSP; P23486; 1QFJ.

HMAP; MF_00430; -; 1.

InterPro; IPR006058; 2Fe2S fd BS.

InterPro; IPR008333; FAD binding_6.

InterPro; IPR001041; Ferredoxin_.

InterPro; IPR001709; FPN cyt_redtse.

InterPro; IPR001433; Oxred_FAD/NAD(P).

Pfam; PF00970; FAD binding_6; 1.

Pfam; PF00111; fer2; 1.

Pfam; PF00175; NAD binding_1; 1.

PRINTS; PR00371; FENCR.

PROSITE; PS00197; 2FE2S FERREDOXIN; FALSE NEG.

KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport; Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;

KW Transmembrane; Inner membrane; Complete proteome.

FT TRANSMEM 2 24 POTENTIAL.

FT DOMAIN 34 114 CATALYTIC.

FT DOMAIN 270 387 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 67 67 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 73 73 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 108 108 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

SQ SEQUENCE 405 AA; 45165 MW; E22DC9CFB7B62B0A CRC64;

Query Match 16.8%; Score 104; DB 1; Length 405;

Best Local Similarity 35.2%; Pred. No. 0.004;

Matches 32; Conservative 14; Mismatches 41; Indels 4; Gaps 4;

QY 8 GTVTIAQTDRYACV-SGESLLAGMAKLGRRGIPVGLNGG-CGVKVRVLRGAVRKLGP 65

Db 32 GUITIKVNGEKELTPAGKLLGALANEG-IFPSACGGSGCGCRVVKSGGGDIL-P 89

QY 66 ISRAHVSAAEENDGYALACRVDPDGDVELEV 96

Db 90 TELSHISKREAREGCKRLSQNVKVTMDIEV 120

RESULT 7

NORF_NEIMA

ID NORF_NEIMA STANDARD; PRT; 405 AA.

AC Q9K0M8;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)


```

DR InterPro: IPR001221; Phe_hydroxylase.
DR Pfam: PF00970; FAD_binding_6; 1.
DR Pfam: PF00111; fer2; 1.
DR Pfam: PF00175; NAD_binding_1; 1.
DR PRINTS: PR00406; CYTBSRDTASE.
DR PRINTS: PR00371; FENCR.
DR PRINTS: PR00410; PHEHYDRXLASE.
DR PROSITE: PS00197; 2FE2S FERREDOXIN; 1.
DR Oxidoreductase; Monooxygenase; NADP; One-carbon metabolism;
KW Electron transport; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Flavoprotein; FAD; 3D-structure.
FT METAL 42 42 IRON-SULFUR (2FE-2S).
FT METAL 47 47 IRON-SULFUR (2FE-2S).
FT METAL 50 50 IRON-SULFUR (2FE-2S).
FT METAL 82 82 IRON-SULFUR (2FE-2S).
FT NP BIND 221 235 FAD (NAD PART) (BY SIMILARITY).
SQ SEQUENCE 348 AA; 38541 MW; 7577BE408CA1CIF CRC64;

Query Match 16.2%; Score 100.5; DB 1; Length 348;
Best Local Similarity 30.0%; Pred. No. 0.0077;
Matches 30; Conservative 12; Mismatches 35; Indels 23; Gaps 5;

Qy 9 TTVTAQDE---RYACVSGSLAGMAKLGRRGIPV--GCLNGGCGVKVRVLRG----- 58
Db 6 TITATDEGSLRECEKSDVDVTAAL---RQIFLMSSCREGGATCALCSEGDYDLK 62

Qy 59 --AVRKLGPISRAHVSBEENDGYALACRVDPGDVELEV 96
Db 63 GCSVOALPP-----EEEGVLVLCRTYPTKTDLEIEL 94

RESULT 9
NORF PASMU STANDARD; PRT; 407 AA.
ID NORF PASMU STANDARD; PRT; 407 AA.
AC Q9CL6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE (Na(+)-translocating NOR subunit F) (Na(+)-NQR subunit F) (NQR complex
DE subunit F) (NQR-1 subunit F).
GN NORF OR PM133.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI TaxID=747;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RT May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to
CC ubiquinol by two successive reactions, coupled with the transport
CC of Na(+) ions from the cytoplasm to the periplasm. The first step
CC is catalyzed by nqrF, which accepts electrons from NADH and
CC reduces ubiquinone-1 to ubiquinol by a one-electron transfer
CC pathway (By similarity).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) +
CC ubiquinol + Na(+) (Out).
CC -!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
CC -!- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE
CC and nqrF (By similarity).
CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).
CC -!- SIMILARITY: Belongs to the nqr family.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/)

```

```

CC or send an email to license@isb-sib.ch.
CC EMBL: AE006171; AAK03417.1; -.
CC HSPSP; P23486; IQFJ.
CC HAMAP; MF_00430; -.
DR InterPro: IPR006058; 2Fe2S fd BS.
DR InterPro: IPR008333; FAD_binding_6.
DR InterPro: IPR001041; Ferredoxin.
DR InterPro: IPR001709; FPN cyt reductase.
DR InterPro: IPR001433; Oxrad_FAD/NAD(P).
DR Pfam: PF00970; FAD_binding_6; 1.
DR Pfam: PF00111; fer2; 1.
DR Pfam: PF00175; NAD_binding_1; 1.
DR PRINTS: PR00371; FENCR.
DR PROSITE: PS00197; 2FE2S FERREDOXIN; FALSE NEG.
DR Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 5 24 POTENTIAL.
FT DOMAIN 34 116 FERREDOXIN.
FT DOMAIN 272 389 CATALYTIC.
FT METAL 69 69 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 75 75 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 78 78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 110 110 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 407 AA; 45252 MW; 9DAC403C9662C8C3 CRC64;

Query Match 16.2%; Score 100; DB 1; Length 407;
Best Local Similarity 32.6%; Pred. No. 0.01;
Matches 31; Conservative 16; Mismatches 38; Indels 10; Gaps 5;

Qy 8 GTVTIAQTDERYACV---SGESLLAGMAKLGRRGIPV--GCLNGG-CGVKVRVLRGAVR 61
Db 32 GDITIEINDPSKAIHLPAAGKLLGALAS---QGIFVSSACGGGSCQCICIVKTEGGGD 88

Qy 62 KLGPISRAHVSBEENDGYALACRVDPGDVELEV 96
Db 89 IL-PTELSHISKREAGCYRLSCQVNVKNSMKVEL 122

RESULT 10
NORF VIBCH STANDARD; PRT; 408 AA.
ID NORF VIBCH STANDARD; PRT; 408 AA.
AC Q9X4Q8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE (Na(+)-translocating NOR subunit F) (Na(+)-NQR subunit F) (NQR complex
DE subunit F) (NQR-1 subunit F).
GN NORF OR VC2290.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI TaxID=666;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=99179036; PubMed=10077658;
RA Haese C.C., Mekalanos J.J.;
RA "Effects of changes in membrane sodium flux on virulence gene
RA expression in Vibrio cholerae.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3183-3187(1999).
RN [2]_
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

```

```

RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483 (2000).
CC -!- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to
CC ubiquinol by two successive reactions, coupled with the transport
CC of Na(+) ions from the cytoplasm to the periplasm. The first step
CC is catalyzed by nqrF, which accepts electrons from NADH and
CC reduces ubiquinone-1 to ubiquinol by a one-electron transfer
CC pathway.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) +
CC ubiquinol + Na(+) (Out).
CC -!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
CC -!- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE
CC and nqrF (By similarity).
CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).
CC -!- SIMILARITY: Belongs to the nqrF family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF117331; AAD29967.1; -.
CC EMBL; AE004300; AAF95434.1; -.
CC F1R; B82094; B82094.
CC HSSP; P33007; 1B9R.
CC TIGR; VC2290; -.
CC HAMAP; MF 00430; -.
CC InterPro; IPR006058; 2Fe2S fd BS.
CC InterPro; IPR008333; FAD_binding_6.
CC InterPro; IPR001041; Ferredoxin.
CC InterPro; IPR001433; Oxred FAD/NAD(P).
CC Pfam; PF00970; FAD binding_6; 1.
CC Pfam; PF00111; fer2; 1.
CC Pfam; PF00175; NAD binding_1; 1.
CC PROSITE; PS00197; 2FE2S_FERREDOXIN; FALSE NEG.
CC Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
CC Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
CC Transmembrane; Inner membrane; Complete proteome.
CC TRANSMEM 5 24
CC DOMAIN 35 117 POTENTIAL.
CC FT DOMAIN 273 390 FERREDOXIN.
CC FT DOMAIN 70 70 CATALYTIC.
CC FT METAL 70 70 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC FT METAL 79 79 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC FT METAL 111 111 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC SEQUENCE 408 AA; 45066 MW; F5665E3623CAAD7B CRC64;
CC
CC Query Match 16.0%; Score 99; DB 1; Length 408;
CC Best Local Similarity 34.4%; Pred. No. 0.013;
CC Matches 32; Conservative 14; Mismatches 41; Indels 6; Gaps 5;
CC
QY 8 GTVTIA-QTDERYACVS--GESILAGMAKLRGRIIPVGLNGG-CGVCKVRVLRGAVRKL 63
DB 33 GDTITSINGDPEKAIYIQPGKLLTALAGAG-VFVSSACGGGSCGQCRVKIKSGGGDIL 91
QY 64 GPISRAHVSAEENDGYALACRVDPGDVLEEV 96
DB 92 -PTDLHISKGEARGERLRACQAVAKMDLLEL 123
CC
RESULT 11
DMPP PSESP
ID DMPP PSESP STANDARD; PRT; 352 AA.
AC P19734;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phenol hydroxylase P5 protein (EC 1.14.13.7) (Phenol 2-monooxygenase

```

```

DE P5 component).
GN DMPP.
OS Pseudomonas sp. (strain CF600).
OG Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072230; PubMed=2254258;
RA Nordlund I., Powlowski J., Shingler V.;
RT "Complete nucleotide sequence and polypeptide analysis of
RT multicomponent phenol hydroxylase from Pseudomonas sp. strain
RT CF600.";
RL J. Bacteriol. 172:6826-6833 (1990).
RN [2]
RP PROBABLE FUNCTION, AND SEQUENCE OF 1-4.
RX MEDLINE=91072231; PubMed=2254259;
RA Powlowski J., Shingler V.;
RT "In vitro analysis of polypeptide requirements of multicomponent
RT phenol hydroxylase from Pseudomonas sp. strain CF600.";
RL J. Bacteriol. 172:6834-6840 (1990).
CC -!- FUNCTION: Catabolizes phenol, and some of its methylated
CC derivatives. P5 is required for growth on phenol, and for
CC in vitro phenol hydroxylase activity.
CC -!- FUNCTION: Probable electron transfer from NADPH, via FAD and the
CC 2Fe-2S center, to the oxygenase activity site of the enzyme.
CC -!- CATALYTIC ACTIVITY: Phenol + NADPH + O(2) = catechol + NADP(+) +
CC H(2)O.
CC -!- COFACTOR: P5 contains a FAD cofactor and a ferredoxin-type 2Fe-2S
CC cluster.
CC -!- PATHWAY: Phenol biodegradation; first step.
CC -!- SUBUNIT: The multicomponent enzyme phenol hydroxylase is formed
CC by P0, P1, P2, P3, P4 and P5 polypeptides.
CC -!- SIMILARITY: In the N-terminal section; belongs to the 2Fe2S plant-
CC type ferredoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M60276; AAA25944.1; -.
CC HSSP; P00235; 1FRF.
CC InterPro; IPR006058; 2Fe2S fd BS.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR008333; FAD_binding_6.
CC InterPro; IPR001041; Ferredoxin.
CC InterPro; IPR001433; Oxred FAD/NAD(P).
CC Pfam; PF00970; FAD binding_6; 1.
CC Pfam; PF00111; fer2; 1.
CC Pfam; PF00175; NAD binding_1; 1.
CC PRINTS; PR00406; CYTB5RDTASE.
CC PRINTS; PR00410; PHEHYDRKLASE.
CC PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
CC Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase;
CC Flavoprotein; FAD; NADP; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
CC Electron transport; Plasmid.
CC INIT MET 0 0
CC FT METAL 36 36 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC FT METAL 44 44 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC SEQUENCE 352 AA; 38346 MW; 1E8B7F6A6A3F12E4 CRC64;
CC
Query Match 15.8%; Score 98; DB 1; Length 352;
CC Best Local Similarity 31.4%; Pred. No. 0.014;
CC Matches 27; Conservative 15; Mismatches 42; Indels 2; Gaps 2;
QY 10 VTIAQTDERYACVSGESILAGMAKLRGRIIPVGLNGGCGVKVRVLRGAVRKLGPISRA 69

```

```

Db      4 VTTEPTGEVIEVDGQTILQAALRQG-VMLPFRACGHGTCTCKQVVEGEV-DIGRASP 61
QY      70 HVSAEENDGYALACRVVPDVELE 95
Db      62 ALMDIERDKVKLACCAIPLSLVIE 87

RESULT 12
ID NQRF VIBAL STANDARD; PRT; 407 AA.
AC Q56584;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE (Na(+)-translocating NADH-quinone reductase subunit beta) (Na(+)-
DE translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex
DE subunit F) (NQR-1 subunit F).
GN NQRF OR NQR6.
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
CX NCBI_TaxID=663;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95246889; PubMed=7729558;
RA Hayashi M., Hirai K., Unemoto T.;
RT "Sequencing and the alignment of structural genes in the nqr operon
RT encoding the Na(+)-translocating NADH-quinone reductase from Vibrio
RT alginolyticus.";
RL FEBS Lett. 363:75-77(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96230452; PubMed=8674603;
RA Tan K., Beattie P., Leach D.R.F., Rich P.R., Coulson A.F.W.,
RA Ward F.B.;
RT "Expression and analysis of the gene for the catalytic beta subunit of
RT the sodium-translocating NADH-ubiquinone oxidoreductase of Vibrio
RT alginolyticus.";
RL Biochem. Soc. Trans. 24:123-12S(1996).
RN [3]
RP SEQUENCE OF 1-10.
RX MEDLINE=98149659; PubMed=9490015;
RA Nakayama Y., Hayashi M., Unemoto T.;
RT "Identification of six subunits constituting Na+-translocating NADH-
RT quinone reductase from the marine Vibrio alginolyticus.";
RL FEBS Lett. 422:240-242(1998).
RN [4]
RP CHARACTERIZATION.
RC STRAIN=DSM 2171;
RX MEDLINE=98055703; PubMed=9395325;
RA Steuber J., Krebs W., Dimroth P.;
RT "The Na+-translocating NADH:ubiquinone oxidoreductase from Vibrio
RT alginolyticus -- redox states of the FAD prosthetic group and
RT mechanism of Ag+ inhibition.";
RL Eur. J. Biochem. 249:770-776(1997).
RN [5]
RP INHIBITION OF ENZYMATIC ACTIVITY.
RA Unemoto T., Ogura T., Hayashi M.;
RT "Modifications by Na+ and K+, and the site of Ag+ inhibition in the
RT Na+-translocating NADH-quinone reductase from a marine Vibrio
RT alginolyticus.";
RL Biochim. Biophys. Acta 1183:201-205(1993).
RN [6]
RP INHIBITION OF ENZYMATIC ACTIVITY.
RX MEDLINE=20016049; PubMed=10549856;
RA Nakayama Y., Hayashi M., Yoshikawa K., Mochida K., Unemoto T.;
RT "Inhibitor studies of a new antibiotic, korormicin, 2-n-heptyl-4-
RT hydroxyquinoline N-oxide and Ag+ toward the Na+-translocating NADH-
RT quinone reductase from the marine Vibrio alginolyticus.";
RL Biol. Pharm. Bull. 22:1064-1067(1999).
RN [7]

```

```

RP REVIEW.
RX MEDLINE=21145117; PubMed=11248187;
RA Hayashi M., Nakayama Y., Unemoto T.;
RT "Recent progress in the Na(+)-translocating NADH-quinone reductase
RT from the marine Vibrio alginolyticus.";
RL Biochim. Biophys. Acta 1505:37-44(2001).
RN [8]
RP REVIEW.
RX MEDLINE=21145118; PubMed=11248188;
RA Steuber J.;
RT "Na(+)-translocation by bacterial NADH:quinone oxidoreductases: an
RT extension to the complex-I family of primary redox pumps.";
RL Biochim. Biophys. Acta 1505:45-56(2001).
CC -I- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to
CC ubiquinol by two successive reactions, coupled with the transport
CC of Na(+) ions from the cytoplasm to the periplasm. The first step
CC is catalyzed by nqrF, which accepts electrons from NADH and
CC reduces ubiquinone-1 to ubiquinol by a one-electron transfer
CC pathway.
CC -I- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) +
CC ubiquinol + Na(+) (Out).
CC -I- COFACTOR: FAD and a 2Fe-2S cluster (Probable).
CC -I- ENZYME REGULATION: ACTIVATED BY NA(+) OR K(+). INHIBITED BY
CC SILVER.
CC -I- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE
CC and nqrF.
CC -I- SUBCELLULAR LOCATION: Inner membrane (Potential).
CC -I- PM: The N-terminus is blocked.
CC -I- SIMILARITY: Belongs to the nqrF family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB008030; BAA22915.1; -.
CC PUR; S65531; S65531.
CC HAMAP; MF_00430; -.
CC InterPro; IPR006058; 2Fe2S_fd_BS.
CC InterPro; IPR008333; FAD_Binding_6.
CC InterPro; IPR001041; Ferredoxin.
CC InterPro; IPR001709; FPN_cyt_reducte.
CC InterPro; IPR001433; Oxred_FAD/NAD(p).
CC Pfam; PF00970; FAD_binding_6; 1.
CC Pfam; PF00111; fer2; 1.
CC Pfam; PF00175; NAD_binding_1; 1.
CC PRINTS; PR00371; FPNCR.
CC PROSITE; PS00197; 2FE2S_FERREDOXIN; FALSE NEG.
CC Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
CC Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
CC Transmembrane; Inner membrane.
CC TRANSMEM 5 24 POTENTIAL.
CC DOMAIN 34 116 FERREDOXIN.
CC DOMAIN 272 389 CATALYTIC.
CC METAL 69 69 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC METAL 75 75 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC METAL 78 78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
CC METAL 110 110 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 407 AA; 45274 MW; A878E99DFCA87346 CRC64;

Query Match 15.8%; Score 98; DB 1; Length 407;
Best Local Similarity 31.2%; Pred. No. 0.016;
Matches 29; Conservative 17; Mismatches 41; Indels 6; Gaps 4;

QY 8 GTVTIAQTDERYACV---SSGLLAGMAKLGRRGIPVCLNGG-CGVCKRVLRGAVKLL 63
Db 32 GDTITSVNDDPSLAITQPGGKLLSALAGAG-VFVSSACGGGCGCQCRVKVSGGGDIL 90
QY 64 GPISFAHVSAEENDGYALACRVVPDVELEV 96

```

Db 91 -PTELDHITKGEAREGERLACQVAMKTDMDIEL 122

RESULT 13

NQRF VIBPA STANDARD; PRT; 407 AA.

AC Q9LCJ0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)

DE (Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex subunit F) (NQR-1 subunit F).

DE NQRF OR NQR6 OR VP2346.

GN Vibrio parahaemolyticus.

OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI_TaxID=670;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RM2210633 / Serotype O3:K6;

RA MEDLINE=22508454; PubMed=12620739;

RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

RA "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism distinct from that of *V. cholerae*.";

RT Lancet 361:743-749 (2003).

RL [2]

RN SEQUENCE OF 72-374 FROM N.A.

RP STRAIN=JCM 2147;

RC MEDLINE=20242140; PubMed=10779868;

RX Kato S., Yumoto I.;

RA "Detection of the Na(+)-translocating NADH-quinone reductase in marine bacteria using a PCR technique.";

RT Can. J. Microbiol. 46:325-332 (2000).

RL -1- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubiquinol by a one-electron transfer pathway.

CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) + ubiquinol + Na(+) (Out).

CC -1- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).

CC -1- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE and nqrF (By similarity).

CC -1- SIMILARITY: Belongs to the nqrF family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF005081; BAC60609.1; -.

DR EMBL; AB024725; BAA83762.1; -.

DR HAMAP; MF_00430; - 1.

DR InterPro; IPR006058; 2Fe2S fd BS.

DR InterPro; IPR008333; FAD_binding_6.

DR InterPro; IPR01041; Ferredoxin.

DR InterPro; IPR001709; FPN cyt reductase.

DR InterPro; IPR001433; Oxid FAD/NAD(P).

DR Pfam; PF00970; FAD binding_6; 1.

DR Pfam; PF00111; fer2; 1.

DR Pfam; PF00175; NAD_binding_1; 1.

DR PRINTS; PR00371; FPNCR.

DR PROSITE; PS00197; 2FE2S FERREDOXIN; FALSE NEG.

DR Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;

KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;

KW Transmembrane; Inner membrane; Complete proteome.

FT TRANSMEM 3 23 POTENTIAL.

FT DOMAIN 34 116 FERREDOXIN.

FT DOMAIN 272 389 CATALYTIC.

FT METAL 69 69 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 75 75 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 78 78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT METAL 110 110 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

FT CONFLICT 114 114 V -> M (IN REF. 2).

FT CONFLICT 185 185 I -> E (IN REF. 2).

FT CONFLICT 278 278 Q -> V (IN REF. 2).

FT CONFLICT 324 326 GLA -> MLQ (IN REF. 2).

SQ SEQUENCE 407 AA; 45083 MW; 747DCC8E9EDBE3A CRC64;

Query Match 15.5%; Score 96; DB 1; Length 407;

Best Local Similarity 31.2%; Pred. No. 0.025; Mismatches 42; Indels 6; Gaps 4;

Matches 29; Conservative 16;

QY 8 GTVTIA--QTDERYACVSGESLLAGNAKLGRGIPVGLNGG-CGVCKVRLGAVRKL 63

DB 32 GDITISVNGDADKAIVTPGGKLLSALAGAG-VFVSSACGGGSGCGCRVKVKSGGDIL 90

QY 64 GPISRAHVSAEEENDGYALACRVVDPGDVELEV 96

DB 91 -PTELDHITKGEAREGERLACQVAMKTDMDIEL 122

RESULT 14

NQRF VIBVU STANDARD; PRT; 407 AA.

AC Q8DBU1;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)

DE (Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex subunit F) (NQR-1 subunit F).

DE NQRF OR VU11826.

GN Vibrio vulnificus.

OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI_TaxID=672;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=CMCP6;

RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.;

RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubiquinol by a one-electron transfer pathway (By similarity).

CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) + ubiquinol + Na(+) (Out).

CC -1- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).

CC -1- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE and nqrF (By similarity).

CC -1- SUBCELLULAR LOCATION: Inner membrane (Potential).

CC -1- SIMILARITY: Belongs to the nqrF family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AB016803; AA010232.1; -.

DR HAMAP; MF_00430; - 1.

```

DR InterPro; IPR006058; 2Fe2s fd BS.
DR InterPro; IPR008333; FAD binding_6.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR001433; Oxid FAD/NAD(P).
DR Pfam; PF00970; FAD binding_6; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR PROSITE; PS00197; 2FE2S FERREDOXIN; FALSE NEG.
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 5 24 Potential.
FT METAL 69 69 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 75 75 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 78 78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 110 110 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 407 AA; 44945 MW; 1FDEC95F196715A2 CRC64;

Query Match 15.5%; Score 96; DB 1; Length 407;
Best Local Similarity 31.2%; Pred. No. 0.025;
Matches 29; Conservative 16; Mismatches 42; Indels 6; Gaps 4;

QY 8 GTVTI---QTDERYACVSGESLLAGMAKLGRRGIPV--GCLNGG-CGVCKVRLGAVRKL 63
Db 32 GDIITISNGDADKSIIVTSPGKLLSALAGAG-VFVSSACGGGSGCGQCRVKVKGSGDIL 90

QY 64 GPISRAHVAEENDGVYALACRVDPDGVLEV 96
Db 91 -PTELDHITKGEAREGERLACQAVKMDMDEL 122

RESULT 15
NORF YERPE
ID NORF YERPE STANDARD; PRT; 407 AA.
AC Q8ZBZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
DE (Na+)-translocating NOR subunit F (Na+)-NOR subunit F) (NOR complex
DE subunit F) (NOR-1 subunit F).
GN NORF OR YPO3235 OR Y0956.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RA "Genome sequence of Versinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.P., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RA "Genome sequence of Versinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
CC -!- FUNCTION: NOR complex catalyzes the reduction of ubiquinone-1 to
CC ubiquinol by two successive reactions, coupled with the transport
CC of Na(+) ions from the cytoplasm to the periplasm. The first step

```

```

is catalyzed by nqrF, which accepts electrons from NADH and
reduces ubiquinone-1 to ubiquinol by a one-electron transfer
pathway (By similarity).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) +
ubiquinol + Na(+) (Out).
-!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
-!- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE
and nqrF (By similarity).
-!- SUBCELLULAR LOCATION: Inner membrane (Potential).
-!- SIMILARITY: Belongs to the nqrF family.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; AJ414156; CAC92470.1; -.
DR EMBL; AE013698; AAM84537.1; -.
DR PIR; AB0393; AB0393.
DR HAWAP; MF_00430; -.
DR InterPro; IPR006058; 2Fe2s fd BS.
DR InterPro; IPR008333; FAD binding_6.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR001709; FPN cyt reductase.
DR InterPro; IPR001433; Oxid FAD/NAD(P).
DR Pfam; PF00970; FAD binding_6; 1.
DR Pfam; PF00111; fer2; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS00197; 2FE2S FERREDOXIN; FALSE NEG.
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 2 24 POTENTIAL.
FT METAL 69 69 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 75 75 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 78 78 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
FT METAL 110 110 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
SQ SEQUENCE 407 AA; 45455 MW; 24AEFDA035483136 CRC64;

Query Match 15.0%; Score 93; DB 1; Length 407;
Best Local Similarity 30.5%; Pred. No. 0.05;
Matches 29; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

QY 8 GTVTI---AQTDERYACVSGESLLAGMAKLGRRGIPV--GCLNGG-CGVCKVRLGAVR 61
Db 32 GDIITVEINEDKSFAPAGDKLL---NMLSSHGIFVSSACGGGSGCGQCRVTKEGGD 88

QY 62 KLGPISRAHVAEENDGVYALACRVDPDGVLEV 96
Db 89 IL-PTLSHISKREAKEGRLACQVNVKQNLKIEL 122

Search completed: August 5, 2004, 13:16:03
Job time : 14 secs

```


Db 61 RKLGPVSRHVSVEEBEAGYSLACRIAPQDVELEVAGKMQKPFRRGFAC 110

RESULT 2

Q9RB86 PRELIMINARY; PRT; 113 AA.

AC Q9RB86

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Chloroplast-type ferredoxin.

GN PHNT2

OS Burkholderia sp. RP007.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Burkholderia.

OX NCBI_TaxID=83784;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RP007;

RX MEDLINE=99382283; PubMed=10448110;

RA Laurie A.D., Lloyd-Jones G.;

RT "Conserved and hybrid meta-cleavage operons from PAH-degrading Burkholderia RP007.";

RL Biochem. Biophys. Res. Commun. 262:308-314(1999).

CC -l- COPACTOR; BINDS 1.2FE-2S CLUSTER (BY SIMILARITY).

DR EMBL; AF112137; AAF02429.1; -.

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR006058; 2Fe2S fd BS.

DR InterPro; IPR001041; Ferredoxin.

DR Pfam; PF00111; fer2; 1.

DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.

KW Iron; Iron-sulfur.

SQ SEQUENCE 113 AA; 11991 MW; 3E7F77A539F77276 CRC64;

Query Match 59.0%; Score 365; DB 2; Length 113;

Best Local Similarity 67.0%; Pred. No. 4.2e-29;

Matches 67; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 10 VTIATDTERYACVSGESLLAGMAKLGRRGIPVGLCLNGCGVCKVRVLRGAVRKLGPISRA 69

Db 12 VTVKQTFGRFSCALGESLLAGMARLGRGIPVGLCLSGCGVCKVACRGSVRKIGAMGRT 71

Qy 70 HVSABEENDGYALACRVVDPDVELEVAGRLRKPFFCGMA 109

Db 72 HISEVEEAQGVVACRVAPTDDELEVGVGKMQKPFKGLS 111

RESULT 3

Q9ZAN6 PRELIMINARY; PRT; 123 AA.

AC Q9ZAN6

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Ferredoxin.

GN CDOT.

OS Comamonas sp. JS765.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Comamonadaceae; Comamonas.

OX NCBI_TaxID=58226;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JS765;

RX MEDLINE=98113817; PubMed=9451836;

RA Parales R.E., Ontl T.A., Gibson D.T.;

RT "Cloning and sequence analysis of a catechol 2,3-dioxygenase gene from the nitrobenzene-degrading strain Comamonas sp JS765.";

RL J. Ind. Microbiol. Biotechnol. 19:385-391(1997)

CC -l- COPACTOR; BINDS 1.2FE-2S CLUSTER (BY SIMILARITY).

DR EMBL; U93090; AAC79917.1; -.

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

Query Match 59.0%; Score 365; DB 2; Length 113;

Best Local Similarity 67.0%; Pred. No. 4.2e-29;

Matches 67; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 10 VTIATDTERYACVSGESLLAGMAKLGRRGIPVGLCLNGCGVCKVRVLRGAVRKLGPISRA 69

Db 12 VTVKQTFGRFSCALGESLLAGMARLGRGIPVGLCLSGCGVCKVACRGSVRKIGAMGRT 71

Qy 70 HVSABEENDGYALACRVVDPDVELEVAGRLRKPFFCGMA 109

Db 72 HISEVEEAQGVVACRVAPTDDELEVGVGKMQKPFKGLS 111

RESULT 4

Q9AE71 PRELIMINARY; PRT; 119 AA.

AC Q9AE71;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Plant-type ferredoxin.

GN TDND1.

OS Pseudomonas putida.

OG Plasmid pTDN1.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=303;

RN [1]

RP SEQUENCE OF 1-29 FROM N.A.

RA Fukumori F., Saint C.P.;

RT "Aniline degradation in Pseudomonas putida UCC22(pTDN1): Initial characterization of its conversion to catechol.";

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 1-29 FROM N.A.

RP MEDLINE=97144524; PubMed=8990291;

RA Fukumori F., Saint C.P.;

RT "Nucleotide sequences and regulational analysis of genes involved in conversion of aniline to catechol in Pseudomonas putida UCC22 (pTDN1).";

RL J. Bacteriol. 179:399-408(1997).

DR EMBL; D85415; BAB62044.1; -.

DR GO; GO:0046821; C:extrachromosomal DNA; IEA.

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR006058; 2Fe2S fd BS.

DR InterPro; IPR001041; Ferredoxin.

DR Pfam; PF00111; fer2; 1.

DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.

KW Iron; Iron-sulfur; Plasmid.

SQ SEQUENCE 119 AA; 12227 MW; 1CDD536BA2C431CE CRC64;

Query Match 58.3%; Score 361; DB 2; Length 119;

Best Local Similarity 63.2%; Pred. No. 1.1e-28;

Matches 74; Conservative 9; Mismatches 26; Indels 8; Gaps 2;

Qy 1 MDAGRVCG--TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGLCLNGCGVCKVRVLRG 58

Db 1 MQATVAVGPSSVCVVQTTGTACSPGESLLRGLRGLRKGIPVGCNGCGVCKVRVIRVG 60

Qy 59 AVRKLGPISRHVSABEENDGYALACRVVDPDVELEVAGRLRKPFFCGMACAGTAA 115

Db 61 CVRALGPVSRHVSABEENDGYALACRVVDPDVELEVAGRLRKPFFCGMACAGTAA 111

RESULT 5

Db 61 RKLGPVSRHVSVEEBEAGYSLACRIAPQDVELEVAGKMQKPFRRGFAC 110

RESULT 2

Q9RB86 PRELIMINARY; PRT; 113 AA.

AC Q9RB86

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Chloroplast-type ferredoxin.

GN PHNT2

OS Burkholderia sp. RP007.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Burkholderia.

OX NCBI_TaxID=83784;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RP007;

RX MEDLINE=99382283; PubMed=10448110;

RA Laurie A.D., Lloyd-Jones G.;

RT "Conserved and hybrid meta-cleavage operons from PAH-degrading Burkholderia RP007.";

RL Biochem. Biophys. Res. Commun. 262:308-314(1999).

CC -l- COPACTOR; BINDS 1.2FE-2S CLUSTER (BY SIMILARITY).

DR EMBL; AF112137; AAF02429.1; -.

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR006058; 2Fe2S fd BS.

DR InterPro; IPR001041; Ferredoxin.

DR Pfam; PF00111; fer2; 1.

DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.

KW Iron; Iron-sulfur.

SQ SEQUENCE 113 AA; 11991 MW; 3E7F77A539F77276 CRC64;

Query Match 59.0%; Score 365; DB 2; Length 113;

Best Local Similarity 67.0%; Pred. No. 4.2e-29;

Matches 67; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 10 VTIATDTERYACVSGESLLAGMAKLGRRGIPVGLCLNGCGVCKVRVLRGAVRKLGPISRA 69

Db 12 VTVKQTFGRFSCALGESLLAGMARLGRGIPVGLCLSGCGVCKVACRGSVRKIGAMGRT 71

Qy 70 HVSABEENDGYALACRVVDPDVELEVAGRLRKPFFCGMA 109

Db 72 HISEVEEAQGVVACRVAPTDDELEVGVGKMQKPFKGLS 111

RESULT 3

Q9ZAN6 PRELIMINARY; PRT; 123 AA.

AC Q9ZAN6

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Ferredoxin.

GN CDOT.

OS Comamonas sp. JS765.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Comamonadaceae; Comamonas.

OX NCBI_TaxID=58226;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JS765;

RX MEDLINE=98113817; PubMed=9451836;

RA Parales R.E., Ontl T.A., Gibson D.T.;

RT "Cloning and sequence analysis of a catechol 2,3-dioxygenase gene from the nitrobenzene-degrading strain Comamonas sp JS765.";

RL J. Ind. Microbiol. Biotechnol. 19:385-391(1997)

CC -l- COPACTOR; BINDS 1.2FE-2S CLUSTER (BY SIMILARITY).

DR EMBL; U93090; AAC79917.1; -.

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

Query Match 59.0%; Score 365; DB 2; Length 113;

Best Local Similarity 67.0%; Pred. No. 4.2e-29;

Matches 67; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 10 VTIATDTERYACVSGESLLAGMAKLGRRGIPVGLCLNGCGVCKVRVLRGAVRKLGPISRA 69

Db 12 VTVKQTFGRFSCALGESLLAGMARLGRGIPVGLCLSGCGVCKVACRGSVRKIGAMGRT 71

Qy 70 HVSABEENDGYALACRVVDPDVELEVAGRLRKPFFCGMA 109

Db 72 HISEVEEAQGVVACRVAPTDDELEVGVGKMQKPFKGLS 111

RESULT 4

Q9AE71 PRELIMINARY; PRT; 119 AA.

AC Q9AE71;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Plant-type ferredoxin.

GN TDND1.

OS Pseudomonas putida.

OG Plasmid pTDN1.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=303;

RN [1]

RP SEQUENCE OF 1-29 FROM N.A.

RA Fukumori F., Saint C.P.;

RT "Aniline degradation in Pseudomonas putida UCC22(pTDN1): Initial characterization of its conversion to catechol.";

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 1-29 FROM N.A.

RP MEDLINE=97144524; PubMed=8990291;

RA Fukumori F., Saint C.P.;

RT "Nucleotide sequences and regulational analysis of genes involved in conversion of aniline to catechol in Pseudomonas putida UCC22 (pTDN1).";

RL J. Bacteriol. 179:399-408(1997).

DR EMBL; D85415; BAB62044.1; -.

DR GO; GO:0046821; C:extrachromosomal DNA; IEA.

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR006058; 2Fe2S fd BS.

DR InterPro; IPR001041; Ferredoxin.

DR Pfam; PF00111; fer2; 1.

DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.

KW Iron; Iron-sulfur; Plasmid.

SQ SEQUENCE 119 AA; 12227 MW; 1CDD536BA2C431CE CRC64;

Query Match 58.3%; Score 361; DB 2; Length 119;

Best Local Similarity 63.2%; Pred. No. 1.1e-28;

Matches 74; Conservative 9; Mismatches 26; Indels 8; Gaps 2;

Qy 1 MDAGRVCG--TVTIAQTDERYACVSGESLLAGMAKLGRRGIPVGLCLNGCGVCKVRVLRG 58

Db 1 MQATVAVGPSSVCVVQTTGTACSPGESLLRGLRGLRKGIPVGCNGCGVCKVRVIRVG 60

Qy 59 AVRKLGPISRHVSABEENDGYALACRVVDPDVELEVAGRLRKPFFCGMACAGTAA 115

Db 61 CVRALGPVSRHVSABEENDGYALACRVVDPDVELEVAGRLRKPFFCGMACAGTAA 111

RESULT 5

DR Pfam: PF00111; fer2; 1.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
KW Iron; Iron-sulfur.
SQ SEQUENCE 121 AA; 12722 MW; C29F512A8BDCC749 CRC64;

Query Match 52.2%; Score 323; DB 2; Length 121;
Best Local Similarity 64.6%; Pred. No. 7.4e-25;
Matches 62; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 10 VTTAQTDERYACVSGESLLAGMAKLGRRGIPVCLNGCGVCKVRLRGAVRKLGPISRA 69
Db 9 VSVETQGTDTYACGTTHESLLSGMLRLGRKGIIPVCGVNGCGVCKVRLRGAVRKLGPISRA 68

QY 70 HVSAAEENDGYALACRVVDPGDVELEVAGRLRKPFF 105
Db 69 HVSDDLQDGYTLACRVAPLEAVRIAVRQRLHKPFF 104

RESULT 7
Q9Z418 PRELIMINARY; PRT; 119 AA.
ID Q9Z418
AC Q9Z418;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ferredoxin.
GN CBZT.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GU31;
RX MEDLINE=99138753; PubMed=9973359;
RA Mars A.E., Kingma J., Kaschabek S.R., Reineke W., Janssen D.B.;
RT "Conversion of 3-chlorocatechol by various catechol 2,3-dioxygenases
RT and sequence analysis of the chlorocatechol dioxygenase region of
RT Pseudomonas putida GU31.";
RL J. Bacteriol. 181:1309-1318(1999).
CC -1- COFACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).
DR EMBL; AF109307; AAD05249.1;
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006058; 2Fe2S fd BS.
DR InterPro; IPR001041; Ferredoxin.
DR Pfam; PF00111; fer2; 1.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
KW Iron; Iron-sulfur.
SQ SEQUENCE 119 AA; 12747 MW; 12256BE66062FF06 CRC64;

Query Match 52.0%; Score 322; DB 2; Length 119;
Best Local Similarity 56.4%; Pred. No. 9.4e-25;
Matches 62; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 9 TTTAQTDERYACVSGESLLAGMAKLGRRGIPVCLNGCGVCKVRLRGAVRKLGPISR 68
Db 10 SVHVMQGTGETTFCPTDESLLQGMRLGRKGIIPVCGVNGCGVCKVRLRGAVRKLGPISR 69

QY 69 AHVSAEENDGYALACRVVDPGDVELEVAGRLRKPFFCGMACAGTAANK 118
Db 70 AHVSAEAEARGTTLACRVAPVTPVQLEVVGFEKVFSGFVSSTNEINK 119

RESULT 8
Q9EXM1 PRELIMINARY; PRT; 91 AA.
ID Q9EXM1
AC Q9EXM1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast-type ferredoxin.
GN ALND.

DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Probable plant-type ferredoxin.
GN	XYLT.
OS	Pseudomonas sp. S-47.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC	Pseudomonadaceae; Pseudomonas.
OX	NCBI_TaxID=115714;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Park D.-W., Kim Y., Lee S.-M., Ka J.-O., Kim C.-K.;
RT	"Cloning and Sequence Analysis of the xylL Gene Responsible for 4CBA-
RT	Dihydrodiol Dehydrogenase from Pseudomonas sp. S-47.";
RL	J. Microbiol. 38:275-280(2000).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Park D.-W., Kim C.-K.;
RL	EMBL: AF320981; AAK08203.2; -.
DR	GO: GO:0005489; F:electron transporter activity; IEA.
DR	GO: GO:0006118; P:electron transport; IEA.
DR	InterPro: IPR006058; 2Fe2S fd BS.
DR	InterPro: IPR001041; Ferredoxin.
DR	Pfam: PF00111; fer2; 1.
DR	PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
KW	Iron; Iron-sulfur.
SQ	SEQUENCE 112 AA; 12054 MW; 799D4F0D36AE226 CRC64;
Query Match 33.2%; Score 205.5; DB 2; Length 112;	
Best Local Similarity 49.4%; Pred.No. 4.5e-13;	
Matches 39; Conservative 14; Mismatches 25; Indels 1; Gaps	
Qy	17 ERVACVSGESLLAGMAKLGRRGIPVGLNGGGCVKRVLRGAVRKLGPIRAHVSAEAE
Db	15 QSFCEAGGQSVLRAMEAQGKRCIPVCGCGGGCLCRVRLSGAYS-GRMSRGHVPAAKA
Qy	77 NDGVVALACRVVDPGDVELE 95
Db	74 AEGFALACVFPQTDLTIE 92
RESULT 14	
Q45344	Q45344 PRELIMINARY; PRT; 119 AA.
ID	Q45344
AC	Q45344
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Chloroplast-type ferredoxin.
GN	TBUW.
OS	Burkholderia pickettii (Pseudomonas pickettii).
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC	Burkholderiaceae; Ralstonia.
OX	NCBI_TaxID=329;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=PK01.
RC	MEDLINE=96209237; PubMed=8633871;
RA	Kukor J.J., Olsen R.H.;
RT	"Catechol 2,3-dioxygenases functional in oxygen-limited (hypoxic)
RT	environments.";
RL	Appl. Environ. Microbiol. 62:1728-1740(1996).
CC	-!- COFACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).
DR	EMBL: U20258; AACL3786.1; -.
DR	GO: GO:0005489; F:electron transporter activity; IEA.
DR	GO: GO:0006118; P:electron transport; IEA.
DR	InterPro: IPR006058; 2Fe2S fd BS.
DR	InterPro: IPR001041; Ferredoxin.
DR	Pfam: PF00111; fer2; 1.
DR	PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
KW	Iron; Iron-sulfur.
SQ	SEQUENCE 119 AA; 13024 MW; 12552001D304F8CE CRC64;

Thu Aug 5 15:10:15 2004

Query Match 32.9%; Score 203.5; DB 2; Length 119;
Best Local Similarity 51.0%; Pred. No. 7.7e-13;
Matches 49; Conservative 6; Mismatches 30; Indels 11; Gaps 3;

QY 28 LAGWAKLGRGIPVGGCLNGGCKVRLGAVRKLKLG-----PISRAHVSAEENDGYAL 82
Db 28 LTGMRLGRKIPVGGCVNGGCKVRLDGSSTR-LGRROPFCPRRRRSA-----GLTL 81
QY 83 ACRRVVPDGVDELEVAGRLRKPFFCGMACAGTAAINK 118
Db 82 ACREAPLTAVRLAVLGRKPKFPRSASAFAGAQSDTK 117

RESULT 15

Q847G8 PRELIMINARY; PRT; 105 AA.
AC Q847G8;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Ferredoxin.
GN NAHT.
OS Pseudomonas putida.
OC Plasmid pDTG1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIB 9816-4;
RA Zylstra G.J., Dennis J.J.;
RT "Complete nucleotide sequence of the NAH plasmid pDTG1 from
Pseudomonas putida NCIB 9816-4.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF491307; AAC64306.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006058; 2Fe2S_fd_BS.
DR InterPro; IPR001041; Ferredoxin.
DR Pfam; PF00111; fer2; 1.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
KW Plasmid.
SQ SEQUENCE 105 AA; 11344 MW; 48568FAC91D640BD CRC64;

Query Match 30.5%; Score 189; DB 2; Length 105;
Best Local Similarity 42.6%; Pred. No. 1.9e-11;
Matches 40; Conservative 16; Mismatches 34; Indels 4; Gaps 2;

QY 10 VTIAQTDERYACVSGESILLAGMAKLGRRGIPVGCCLNGGCKVRLGAVRKLGPISRA 69
Db 7 ITVQGGGERFACQPLQSVLSAMETQKQCLFVCGCGGGLCKVRVLADY-ECGRVSCK 65
QY 70 HVSAREENDGYALACRVDPDGDVELEVAGRLRKP 103
Db 66 HLPVEAREQGYALACRLPARSDLCIE---RYSKP 96

Search completed: August 5, 2004, 13:16:54
Job time : 40 secs